

Best Local Similarity 36.7%; Pred. No. 16; Mismatches 8; Gaps 2;  
Matches 18; Conservative 19; Indels 4; Gaps 2;  
2 NGFASLRRNQFII---LVFLFLQIQSLG-LDIDSPTAEVCATHITSP 46  
10 NVIVGLFRKTSLLITSLIGLGLSLGVLGDLGNLARAETKATNPSP 58  
RESULT 3  
370100  
phosphoglucosyltransferase (femD) homolog - Lyme disease spirochete  
Species: Borrelia burgdorferi (Lyme disease spirochete)  
Date: 13-Feb-1998 #sequence\_revision 13-Feb-1998 #text\_change 08-Oct-1999  
Accession: D70100  
Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; White  
son, D.; Peterson, J.J.; Kurland, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt,  
Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.  
Nature 390, 580-586, 1997  
Authors: Smith, H.O.; Venter, J.C.  
Title: Genomic sequence of a Lyme disease spirochete, Borrelia burgdorferi.  
Reference number: A70100; MUID:98055943; PMID:9403685  
Accession: D70100  
Status: preliminary; nucleic acid sequence not shown; translation not shown  
Molecule type: DNA  
Residues: 1-597 <KLE>  
Cross-references: GB:AE001115; GB:AE000783; NID:g2687879; PIDN:AAC66399.1; PID:g268788  
Experimental source: strain B31  
Query Match 23.0%; Score 52.5; DB 2; Length 597;  
Best Local Similarity 33.3%; Pred. No. 29; Mismatches 6; Gaps 1;  
Matches 13; Conservative 11; Indels 9; Gaps 1;  
QY 15 LVFLFLQIQS-----LGLDIDSRPTAEVCATHI 44  
DB 50 LIALIIFISNVFNESKPIYGLDLSRPTGNTIAETII 88  
RESULT 4  
T03488  
glutamate-tRNA ligase (EC 6.1.1.17) - Rhodobacter capsulatus  
Species: Rhodobacter capsulatus  
Date: 24-Mar-1999 #sequence\_revision 24-Mar-1999 #text\_change 03-Jun-2002  
Accession: T03488  
R.Vlcek, C.; Paces, V.; Maltsev, N.; Paces, J.; Hasek, R.; Fomstein, M.  
Proc. Natl. Acad. Sci. U.S.A. 94, 9384-9388, 1997  
Title: Sequence of a 189-kb segment of the chromosome of Rhodobacter capsulatus SB1003  
Reference number: Z14955; MUID:97404404; PMID:9256491  
Accession: T03488  
Status: preliminary; translated from GB/EMBL/DBJ  
Molecule type: DNA  
Residues: 1-137 <VLC>  
Cross-references: EMBL:AF010496; NID:g3128256; PIDN:AAC16141.1; PID:g3128289  
Genetics:  
Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis  
A:Map position: 1  
Query Match 22.8%; Score 52; DB 2; Length 137;  
Best Local Similarity 30.0%; Pred. No. 8.2; Mismatches 11; Indels 6; Gaps 2;  
Matches 12; Conservative 11; Indels 11; Gaps 2;  
QY 8 LRRNQFI-LVFLFLQIQSLGLDIDSRPTAEVCATHITSP 46  
DB 1 MKRRFTEAQIIGMIKEQAGL-----PTSLCRKHGLSP 35  
RESULT 5  
C82713  
polysaccharide biosynthetic protein Xfl183 [imported] - Xylella fastidiosa (strain 945c)  
Species: Xylella fastidiosa  
Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 02-Sep-2000  
Accession: C82713  
Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen  
Nature 406, 151-157, 2000

A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.  
A:Reference number: A8515; MUID:20365717; PMID:10910347  
A:Note: for a complete list of authors see reference number A59328 below  
Accession: C82713  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-433 <8IM>  
A:Cross-references: GB:AE003952; GB:AE003849; NID:g9106147; PIDN:AAF83993.1; GSPDB:GN001  
A:Experimental source: strain 945c  
R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvaranga, R.; A  
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H  
as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.  
submitted to GenBank, June 2000  
Authors: Ferreira, V.C.A.; Perro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm  
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigr  
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E  
A:Authors: Martins, E.V.F.; Matsukuma, A.V.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.,  
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.  
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.B.; de Sa, R.G.; Santelli, R.V.; Sawasak  
A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir  
M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z  
A:Reference number: A59328  
A:Contents: annotation  
C:Genetics:  
A:Gene: Xfl183  
C:Superfamily: UDP-N-acetyl-D-mannosaminuronic acid dehydrogenase  
Query Match 22.8%; Score 52; DB 2; Length 433;  
Best Local Similarity 41.9%; Pred. No. 25; Mismatches 13; Conservative 14; Indels 0; Gaps 0;  
QY 15 LVFLFLQIQSLGLDIDSRPTAEVCATHITIS 45  
DB 29 LAVAFGRFTLGFIDICRVQOLCAGHDIT 59  
RESULT 6  
C86206  
hypochemical protein [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Mar-2001  
Accession: C86206  
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,  
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.,  
anser, N.F.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000  
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C  
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luo, J.S.; Maiti, R.; Marziani,  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A:Reference number: A86141; MUID:21016719; PMID:11130712  
Accession: C86206  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-155 <STO>  
A:Cross-references: GB:AE005172; NID:g8954033; PIDN:AAF82207.1; GSPDB:GN00141  
C:Genetics:  
A:Map position: 1  
Query Match 22.8%; Score 51.5; DB 2; Length 155;  
Best Local Similarity 33.3%; Pred. No. 11; Mismatches 13; Conservative 7; Indels 1; Gaps 1;  
Matches 13; Conservative 7; Indels 18; Gaps 1;  
QY 8 LRRNQFILLVFLFLQIQSLGLDIDSRPTAEVCATHITSP 46  
DB 3 LRRVWLYLFLFHQLNLPVSSRPS-VDNTHETLP 40  
RESULT 7  
AG2775  
protein-export membrane protein SPC [imported] - Agrobacterium tumefaciens (strain C58,

A;Residues: 1-328 <PAR>  
A;Cross-references: GB:AL162752; GB:AL157959; PIDN:CAB83372.1; PID:g737878  
A;Experimental source: serogroup A, strain Z2491  
C;Genetics:  
A;Gene: NMA0055  
C;Superfamily: Neisseria meningitidis probable integral membrane protein NMA0055

Query Match 22.4%; Score 51; DB 2; Length 328;  
Best Local Similarity 44.7%; Pred. No. 26;  
Matches 17; Conservative 4; Mismatches 11; Indels 6; Gaps 1;

QY 10 RNQFILLVFL-----QIQSLGLDIDSRPTAEVCAT 41  
|||:|||  
Db 99 RNTLLLVLSLAFIWSAQITLALSMFAVAVVAT 136  
|||:|||

RESULT 10  
E81225  
hypothetical protein NM0213 [imported] - Neisseria meningitidis (strain MC58 serogroup B)  
C;Species: Neisseria meningitidis  
C;Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 19-Jan-2001  
A;Accession: E81225  
R;Tetelin H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.F.; Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; Qin, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M.  
Science 287, 1809-1815, 2000  
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Frazer, C.M.; Moxon, E.R.; Rappuoli, R.; Veith, R.T.  
A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.  
A;Reference number: AB1000; UID:20175755; PMID:10710307  
A;Accession: E81225  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-328 <T>  
A;Cross-references: GB:AE002378; GB:AE002098; NID:g7225428; PIDN:AAP40669.1; PID:g7225428  
A;Experimental source: serogroup B, strain MC58  
C;Genetics:  
A;Gene: NMB0213  
C;Superfamily: Neisseria meningitidis probable integral membrane protein NMA0055

Query Match 22.4%; Score 51; DB 2; Length 328;  
Best Local Similarity 44.7%; Pred. No. 26;  
Matches 17; Conservative 4; Mismatches 11; Indels 6; Gaps 1;

QY 10 RNQFILLVFL-----QIQSLGLDIDSRPTAEVCAT 41  
|||:|||  
Db 99 RNTLLLVLSLAFIWSAQITLALSMFAVAVVAT 136  
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RESULT 11  
T28826  
Hypothetical protein F20B4.2 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 18-Feb-2000  
A;Accession: T28826  
R;Stelljes, L.  
submitted to the EMBL Data Library, May 1996  
A;Description: The sequence of C. elegans cosmid F20B4.  
A;Reference number: Z20529  
A;Accession: T28826  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-337 <STE>  
A;Cross-references: EMBL:U58735; PIDN:AAC48143.1; GSPDB:GN00028; CESP:F20B4.2  
A;Experimental source: strain Bristol N2; clone F20B4  
C;Genetics:  
A;Gene: CESP:F20B4.2  
A;Map position: X

Query Match 22.4%; Score 51; DB 2; Length 337;  
Best Local Similarity 32.1%; Pred. No. 27;  
Matches 9; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

QY 17 VLFLQLQISLGLDIDSRPTAEVCATHI 44

A;Species: Agrobacterium tumefaciens  
C;Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 18-Nov-2002  
A;Accession: AG2775  
Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.; Prange, G.; Gillet, W.; Grant, C.; Guentherer, D.; Kutayavin, T.; Levy, R.; Li, M.; McClellan, Karp, P.; Romero, P.; Zhang, S.  
Science 294, 2317-2323, 2001  
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krepan, W.; Perry, M.; Gordon-Kamm, Uger, E.W.  
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.  
A;Reference number: AB2577; UID:21608550; PMID:11743193  
A;Accession: AG2775  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-157 <KUR>  
A;Cross-references: GB:AE008638; PIDN:AAL42621.1; PID:g17740050; GSPDB:GN00186  
A;Experimental source: strain C58 (Dupont)  
C;Genetics:  
A;Gene: secG  
A;Map position: circular chromosome

Query Match 22.4%; Score 51; DB 2; Length 157;  
Best Local Similarity 45.7%; Pred. No. 13;  
Matches 16; Conservative 2; Mismatches 15; Indels 2; Gaps 1;

QY 3 GPASLRNRQIFLLVLFIQISGL--DIISRPT 35  
|||:|||  
Db 43 GTANALRTTGILAAFLFSLGLGLMTWRYESRPT 77  
|||:|||

RESULT 8  
397555  
hypothetical protein AGR\_C\_2986 [imported] - Agrobacterium tumefaciens (strain C58, Cerevisiae)  
C;Species: Agrobacterium tumefaciens  
C;Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 18-Nov-2002  
A;Accession: E97555  
A;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Hollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001  
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tumefaciens  
A;Reference number: A97359; UID:21608551; PMID:11743194  
A;Accession: E97555  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-162 <KUR>  
A;Cross-references: GB:ABC07869; PIDN:AAK87398.1; PID:g15156708; GSPDB:GN00169  
C;Genetics:  
A;Gene: AGR\_C\_2986  
A;Map position: circular chromosome

Query Match 22.4%; Score 51; DB 2; Length 162;  
Best Local Similarity 45.7%; Pred. No. 13;  
Matches 16; Conservative 2; Mismatches 15; Indels 2; Gaps 1;

QY 3 GPASLRNRQIFLLVLFIQISGL--DIISRPT 35  
|||:|||  
Db 48 GTANALRTTGILAAFLFSLGLGLMTWRYESRPT 82  
|||:|||

RESULT 9  
H81996  
probable integral membrane protein NMA0055 [imported] - Neisseria meningitidis (strain Z2491)  
C;Species: Neisseria meningitidis  
C;Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 02-Feb-2001  
A;Accession: H81996  
R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel, R.; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, Nature 404, 502-506, 2000  
A;Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.  
A;Reference number: AB1775; UID:2022556; PMID:10761919  
A;Accession: H81996  
A;Status: preliminary  
A;Molecule type: DNA



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CM protein - protein search, using sw model

Run on: March 8, 2004, 12:07:46 ; Search time 11.9559 Seconds  
(without alignments)  
198.629 Million cell updates/sec

Title: US-09-600-932-2\_COPY\_1\_46  
Perfect score: 228  
Sequence: 1 MNGFASLLRNQFLLVLEL.....GLDIDSRPAEYCAHTTISP 46

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: /cgn2\_6/ptodata/2/iaa/5B COMB.pcp.\*  
3: /cgn2\_6/ptodata/2/iaa/6A COMB.pcp.\*  
4: /cgn2\_6/ptodata/2/iaa/6B COMB.pcp.\*  
5: /cgn2\_6/ptodata/2/iaa/PTUS COMB.pcp.\*  
6: /cgn2\_6/ptodata/2/iaa/backfiles1.pcp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	57.5	22.2	249	4	US-09-489-039A-13124 Sequence 13124, A
2	52	22.8	65	3	US-08-905-223-453 Sequence 453, App
3	52	22.8	123	3	US-08-938-548B-10 Sequence 10, Appl
4	52	22.8	123	4	US-08-939-093A-10 Sequence 10, Appl
5	52	22.8	123	4	US-08-211-823C-10 Sequence 10, Appl
6	52	22.8	130	3	US-08-938-548B-6 Sequence 6, Appl
7	52	22.8	130	4	US-08-939-093A-6 Sequence 6, Appl
8	52	22.8	130	4	US-08-230-896C-1 Sequence 1, Appl
9	52	22.8	130	4	US-08-230-896C-2 Sequence 2, Appl
10	52	22.8	130	4	US-09-211-823C-6 Sequence 6, Appl
11	52	22.8	162	4	US-08-663-600A-126 Sequence 126, App
12	52	22.8	162	4	US-08-663-600A-220 Sequence 220, App
13	52	22.8	163	4	US-08-149-476-462 Sequence 462, App
14	51.5	22.6	300	4	US-08-252-991A-27295 Sequence 27295, A
15	50	21.9	416	4	US-08-489-039A-13278 Sequence 13278, A
16	48.5	21.3	681	4	US-09-252-991A-18889 Sequence 18889, A
17	48	21.1	232	4	US-09-134-001C-4874 Sequence 4874, Ap
18	48	21.1	424	4	US-09-252-991A-18895 Sequence 18895, A
19	48	21.1	618	4	US-08-134-000C-6538 Sequence 6538, Ap
20	47.5	20.8	318	1	US-08-537-942A-1 Sequence 1, Appl
21	47.5	20.8	318	3	US-08-997-252A-1 Sequence 1, Appl
22	47.5	20.8	318	4	US-09-517-739-1 Sequence 1, Appl
23	47.5	20.8	318	4	US-09-935-720A-1 Sequence 1, Appl
24	47.5	20.8	362	4	US-09-485-648-6 Sequence 6, Appl
25	47.5	20.8	362	4	US-09-503-565-6 Sequence 6, Appl
26	47.5	20.8	362	4	US-09-485-649-6 Sequence 6, Appl
27	47.5	20.8	423	4	US-09-252-991A-32616 Sequence 32616, A

28	47.5	20.8	718	4	US-09-252-991A-28229 Sequence 28229, A
29	47.5	20.8	1139	1	US-08-537-210A-4 Sequence 4, Appl
30	47.5	20.8	1139	3	US-09-113-825-4 Sequence 4, Appl
31	47.5	20.8	2703	1	US-08-185-432-19 Sequence 19, Appl
32	47.5	20.8	2703	4	US-08-899-232-4 Sequence 4, Appl
33	47	20.6	84	4	US-09-543-681A-7825 Sequence 7825, Ap
34	46.5	20.4	434	4	US-09-543-681A-6266 Sequence 6266, Ap
35	46.5	20.4	506	4	US-09-134-001C-4282 Sequence 4282, Ap
36	46.5	20.4	577	4	US-09-489-039A-12056 Sequence 12056, A
37	46	20.2	51	4	US-09-482-273-168 Sequence 168, App
38	46	20.2	81	4	US-09-482-273-262 Sequence 262, App
39	46	20.2	260	3	US-08-957-130-15 Sequence 15, Appl
40	46	20.2	277	4	US-09-252-991A-18435 Sequence 18435, A
41	46	20.2	281	3	US-08-808-148-4 Sequence 4, Appl
42	46	20.2	1044	4	US-09-252-991A-24495 Sequence 24495, A
43	45.5	20.0	197	4	US-08-252-991A-31560 Sequence 31560, A
44	45.5	20.0	445	4	US-09-134-001C-3507 Sequence 3507, Ap
45	45	19.7	69	4	US-09-107-532A-6826 Sequence 6826, Ap

ALIGNMENTS

RESULT 1  
US-09-489-039A-13124  
; Sequence 13124, Application US/09489039A  
; Patent No. 6610836  
; GENERAL INFORMATION:  
; APPLICANT: Gary Breton et. al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
; FILE REFERENCE: 2709.2004001  
; CURRENT APPLICATION NUMBER: US/09/489,039A  
; CURRENT FILING DATE: 2000-01-27  
; PRIOR APPLICATION NUMBER: US 60/117,747  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 14342  
; SEQ ID NO 13124  
; LENGTH: 249  
; TYPE: PRT  
; ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-13124

Query Match 25.2%; Score 57.5; DB 4; Length 249;  
Best Local Similarity 35.8%; Pred. No. 0.6; 16; Indels 1; Gaps 1;  
Matches 14; Conservative 8; Mismatches 16

QY 4 FASLLRNQFLLVLEL-LQIQLGLDIDSRPAEYCAT 41  
DB 88 YISLARATPLVTLVLELFLSLPTMGINKVAAIVALT 126

RESULT 2  
US-08-905-223-453  
; Sequence 453, Application US/08905223  
; Patent No. 6222029  
; GENERAL INFORMATION:  
; APPLICANT: Edwards, Jean-Baptiste D.  
; APPLICANT: Duclert, Aymeric  
; APPLICANT: Lacroix, Bruno  
; TITLE OF INVENTION: 5' ESTS FOR SECRETED PROTEINS  
; NUMBER OF SEQUENCES: 503  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Knobbe, Martena, Olson & Bear  
; STREET: 501 West Broadway  
; CITY: San Diego  
; STATE: California  
; COUNTRY: USA  
; ZIP: 92101-3505  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy Disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: Win95



;; SOFTWARE: Word  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/905,223  
;; FILING DATE:  
;; CLASSIFICATION: 536  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Israelsen, Ned A.  
;; REGISTRATION NUMBER: 29,655  
;; REFERENCE/DOCKET NUMBER:  
;; TELEPHONE: (619) 235-8550  
;; TELEFAX: (619) 235-0176  
;; INFORMATION FOR SEQ ID NO: 453:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 65 amino acids  
;; TYPE: AMINO ACID  
;; TOPOLOGY: LINEAR  
;; MOLECULE TYPE: PROTEIN  
;; ORIGINAL SOURCE:  
;; ORGANISM: Homo Sapiens  
;; TISSUE TYPE: Brain  
;; FEATURE:  
;; NAME/KEY: sig\_peptide  
;; LOCATION: -21...-1  
;; IDENTIFICATION METHOD: Von Heijne matrix  
;; OTHER INFORMATION: score 5.6  
;; OTHER INFORMATION: seq LVLSLQLFLLSYD/LF  
US-08-905-223-453

Query Match 22.8%; Score 52; DB 3; Length 65;  
Best Local Similarity 45.5%; Pred. No. 0.77;  
Matches 10; Conservative 6; Mismatches 6; Indels 6; Gaps 0;

QY 1 MNGFASLLRRNQFILLVFLFIQ 22  
Db 24 VNSFSELIQKTPVQLVFLFIQ 45

RESULT 3  
US-08-938-548B-10  
; Sequence 10, Application US/08938548B  
; Patent No. 6001963  
; GENERAL INFORMATION:  
; APPLICANT: Yanagisawa, Masaaki  
; APPLICANT: Bergsma, Derk  
; APPLICANT: Wilson, Shelagh  
; APPLICANT: Brooks, David  
; APPLICANT: Gellai, Miklos  
; TITLE OF INVENTION: NOVEL LIGANDS OF THE NEUROPEPTIDE  
; TITLE OF INVENTION: RECEPTOR HFGAN72  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corporation  
; STREET: 709 Swedeland Road  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: United States of America  
; ZIP: 19406  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/938,548B  
; FILING DATE: 26-SEPT-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/887,382  
; FILING DATE: 2-JUL-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/820,519  
; FILING DATE: 19-MAR-1997

;; APPLICATION NUMBER: 60/033,604  
;; FILING DATE: 17-DEC-1997  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Elizabeth J. Hecht  
;; REGISTRATION NUMBER: 41,824  
;; REFERENCE/DOCKET NUMBER: ATG50037-2  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 610-270-5009  
;; TELEFAX: 610-270-5090  
;; TELEX:  
;; INFORMATION FOR SEQ ID NO: 10:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 123 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
US-08-938-548B-10  
Query Match 22.8%; Score 52; DB 3; Length 123;  
Best Local Similarity 38.7%; Pred. No. 1.8;  
Matches 12; Conservative 5; Mismatches 14; Indels 0; Gaps 0;

QY 15 LVLFLLIQSLGLDIDSRPTAEVCATHTIS 45  
Db 8 LLLLLLPPALLSLGVDAPLPDCCQKTC 38

RESULT 4  
US-08-939-093A-10  
; Sequence 10, Application US/08939093A  
; Patent No. 630854  
; GENERAL INFORMATION:  
; APPLICANT: Yanagisawa, Masaaki  
; APPLICANT: Bergsma, Derk  
; APPLICANT: Wilson, Shelagh  
; APPLICANT: Brooks, David  
; APPLICANT: Gellai, Miklos  
; TITLE OF INVENTION: NOVEL LIGANDS OF THE NEUROPEPTIDE  
; TITLE OF INVENTION: RECEPTOR HFGAN72  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corporation  
; STREET: 709 Swedeland Road  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: United States of America  
; ZIP: 19406  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/939,093A  
; FILING DATE: 26-SEPT-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/887,382  
; FILING DATE: 2-JUL-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/820,519  
; FILING DATE: 19-MAR-1997  
; APPLICATION NUMBER: 60/033,604  
; FILING DATE: 17-DEC-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: King, William T.  
; REGISTRATION NUMBER: 30,954  
; REFERENCE/DOCKET NUMBER: ATG50037-3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 610-270-5219  
; TELEFAX: 610-270-4026  
; TELEX:

INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 123 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Protein  
US-08-939-093A-10

Query Match 22.8%; Score 52; DB 4; Length 123;  
Best Local Similarity 38.7%; Pred. No. 1.8;  
Matches 12; Conservative 5; Mismatches 14; Indels 0; Gaps 0;

QY 15 LVLFLQLQISGLDIDSRPTAEVCATHIS 45  
DB 8 LLLLLLPPALLSLGVDAQPLDCCCRQKTC 38

## RESULT 5

US-09-211-823C-10  
Sequence 10, Application US/09211823C  
Patent No. 6664229  
GENERAL INFORMATION:  
APPLICANT: HAGEN, JAMES JOSEPH  
APPLICANT: TERRETT, JONATHAN ALEXANDER  
APPLICANT: UPTON, NEIL  
APPLICANT: PIPER, DAVID  
APPLICANT: SMITH, MARTIN IAN  
APPLICANT: KENNETH, GUY ANTHONY  
APPLICANT: PATEL, SARASWATI K.  
TITLE OF INVENTION: METHODS OF TREATMENT USING NOVEL LIGANDS  
TITLE OF INVENTION: OF THE NEUROPEPTIDE RECEPTOR HFGAN72 AND AGONISTS OR  
TITLE OF INVENTION: ANTAGONISTS THEREOF  
FILE REFERENCE: P50745  
CURRENT APPLICATION NUMBER: US/09/211,823C  
PRIOR FILING DATE: 1998-12-15  
PRIOR APPLICATION NUMBER: US 60/069,459  
PRIOR FILING DATE: 1997-12-15  
PRIOR APPLICATION NUMBER: US 60/069,785  
PRIOR FILING DATE: 1997-12-16  
NUMBER OF SEQ ID NOS: 23  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 10  
LENGTH: 123  
TYPE: PRT  
ORGANISM: MUS MUSCULUS  
US-09-211-823C-10

Query Match 22.8%; Score 52; DB 4; Length 123;  
Best Local Similarity 38.7%; Pred. No. 1.8;  
Matches 12; Conservative 5; Mismatches 14; Indels 0; Gaps 0;

QY 15 LVLFLQLQISGLDIDSRPTAEVCATHIS 45  
DB 8 LLLLLLPPALLSLGVDAQPLDCCCRQKTC 38

## RESULT 6

US-08-938-548B-6  
Sequence 6, Application US/08938548B  
Patent No. 6001963  
GENERAL INFORMATION:  
APPLICANT: Yanagisawa, Masashi  
APPLICANT: Bergsma, Derk  
APPLICANT: Wilson, Shelagh  
APPLICANT: Brooks, David  
APPLICANT: Gellai, Miklos  
TITLE OF INVENTION: NOVEL LIGANDS OF THE NEUROPEPTIDE  
TITLE OF INVENTION: RECEPTOR HFGAN72  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SmithKline Beecham Corporation  
STREET: 709 Swedeland Road

CITY: King of Prussia  
STATE: PA  
COUNTRY: United States of America  
ZIP: 19406  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/938,548B  
FILING DATE: 26-SEPT-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/887,382  
FILING DATE: 2-JUL-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/820,519  
FILING DATE: 19-MAR-1997  
APPLICATION NUMBER: 60/033,604  
FILING DATE: 17-DEC-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Elizabeth J. Hecht  
REGISTRATION NUMBER: 41,824  
REFERENCE/DOCKET NUMBER: ATGS0037-2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 610-270-5009  
TELEFAX: 610-270-5090  
TELEX:

INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 130 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Protein  
US-08-938-548B-6

Query Match 22.8%; Score 52; DB 3; Length 130;  
Best Local Similarity 38.7%; Pred. No. 1.9;  
Matches 12; Conservative 5; Mismatches 14; Indels 0; Gaps 0;

QY 15 LVLFLQLQISGLDIDSRPTAEVCATHIS 45  
DB 15 LLLLLLPPALLSLGVDAQPLDCCCRQKTC 45

## RESULT 7

US-08-939-093A-6  
Sequence 6, Application US/08939093A  
Patent No. 6309854  
GENERAL INFORMATION:  
APPLICANT: Yanagisawa, Masashi  
APPLICANT: Bergsma, Derk  
APPLICANT: Wilson, Shelagh  
APPLICANT: Brooks, David  
APPLICANT: Gellai, Miklos  
TITLE OF INVENTION: NOVEL LIGANDS OF THE NEUROPEPTIDE  
TITLE OF INVENTION: RECEPTOR HFGAN72  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SmithKline Beecham Corporation  
STREET: 709 Swedeland Road  
CITY: King of Prussia  
STATE: PA  
COUNTRY: United States of America  
ZIP: 19406  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:

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/ APPLICATION NUMBER: US/08/939,093A
/ FILING DATE: 26-SEPT-1997
/ CLASSIFICATION: 536
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/887,382
/ FILING DATE: 2-JUL-1997
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/820,519
/ FILING DATE: 19-MAR-1997
/ APPLICATION NUMBER: 60/033,604
/ FILING DATE: 17-DEC-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: King, William T.
/ REGISTRATION NUMBER: 30,954
/ REFERENCE/DOCKET NUMBER: ATG50037-3
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 610-270-5219
/ TELEFAX: 610-270-4026
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 6:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 130 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-939-093A-6

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Query Match 22.8%; Score 52; DB 4; Length 130;  
Best Local Similarity 38.7%; Pred. No. 1.9;  
Matches 12; Conservative 5; Mismatches 14; Indels

QY 15 LVLFLQLQSLGLDIDSRPTAEVCATHITIS 45  
||: || | | : : : | | |  
pb 15 LLLLLPALLSLGVDAOPLPDCCKTCS 45

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RESULT 8
US-09-230-896C-1
; Sequence 1, Application US/09230896C
; Patent No. 6635479
; GENERAL INFORMATION:
; APPLICANT: The Scripps Research Institute
; APPLICANT: Sutcliffe, et al.
; TITLE OF INVENTION: Hypothalamus-Specific Polypeptides
; FILE REFERENCE: TSI-548.1
; CURRENT APPLICATION NUMBER: US/09/230,896C
; CURRENT FILING DATE: 1999-02-02
; PRIOR APPLICATION NUMBER: 60/023,220
; PRIOR FILING DATE: 1996-08-02
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 130
; TYPE: PRT
; ORGANISM: ratus ratus
; US-09-230-896C-1

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Query Match 22.8%; Score 52; DB 4; Length 130;  
Best Local Similarity 38.7%; Pred. No. 1.9;  
Matches 12; Conservative 5; Mismatches 14; Indels

Qy 15 LVLFLQLQISGLDIDSRPTAEVCATHIS 45  
||: || | | : : | |  
Nb 15 LLLLLPPALISGLVDAOPLDCCROKICS 45

RESULT 9  
US-09-230-896C-2  
; Sequence 2, Application US/09230896C  
; Patent No. 6635479  
; GENERAL INFORMATION:  
; APPLICANT: The Scripps Research Institute

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/ APPLICANT: Sutcliffe, et al.
/ TITLE OF INVENTION: Hypothalamus-Specific Polypeptides
/ FILE REFERENCE: TSRI-548.1
/ CURRENT APPLICATION NUMBER: US/09/230,896C
/ CURRENT FILING DATE: 1999-02-02
/ PRIOR APPLICATION NUMBER: 60/023,220
/ PRIOR FILING DATE: 1996-08-02
/ NUMBER OF SEQ ID NOS: 29
/ SOFTWARE: fastseq for Windows Version 4.0
/ SEQ ID NO 2
/ LENGTH: 130
/ TYPE: PRT
/ ORGANISM: mus musculus
/ US-09-230-896C-2

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Query Match 22.8%; Score 52; DB 4; Length 130;  
Best Local Similarity 38.7%; Pred. No. 1.9;  
Matches 12: Conservative 5; Mismatches 14; Indels

QY 15 LVLVLLQIQSLGLDIDSRPTAEVCATHTIS 45  
|||: ||| | : : :  
Db 15 LMLLILLPPALLSLGVDAOPLPDCROKTCIS 45

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RESULT 10
US-09-211-823C-6
; Sequence 6, Application US/09211823C
; Patent No. 6664229
; GENERAL INFORMATION:
; APPLICANT: HAGEN, JAMES JOSEPH
; APPLICANT: TERRETT, JONATHAN ALEXANDER
; APPLICANT: UPTON, NEIL
; APPLICANT: PIPER, DAVID
; APPLICANT: SMITH, MARTIN IAN
; APPLICANT: KENNETT, GUY ANTHONY
; APPLICANT: PATEL, SARASWATI R.
; TITLE OF INVENTION: METHODS OF TREATMENT USING NOVEL LIGANDS
; TITLE OF INVENTION: OF THE NEUROPEPTIDE RECEPTOR HFGAN72 AND AGONISTS OR
; TITLE OF INVENTION: ANTAGONISTS THEREOF
; FILE REFERENCE: P50745
; CURRENT APPLICATION NUMBER: US/09/211,823C
; CURRENT FILING DATE: 1998-12-15
; PRIOR APPLICATION NUMBER: US 60/069,459
; PRIOR FILING DATE: 1997-12-15
; PRIOR APPLICATION NUMBER: US 60/069,785
; PRIOR FILING DATE: 1997-12-16
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 130
; TYPE: PRT
; ORGANISM: RATTUS RATTUS
; US-09-211-823C-6

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Query Match 22.8%; Score 52; DB 4; Length 130;  
Best Local Similarity 38.7%; Pred. No. 1.9;  
Matches 12: Conservative 5; Mismatches 14; Indels

Qy 15 LLVFLQLQSLGLDIDSRPTAEVCATHITIS 45  
||: || | | | : : : | | |  
nb 15 LLVFLQPAALSLGVDAOPLDPCROKTCIS 45

RESULT 11  
US-09-663-600A-126  
; Sequence 126, Application US/09663600A  
; Patent No. 6573068  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Wilne Edwards, Jean-Baptiste  
; APPLICANT: Duclert, Aymeric  
; APPLICANT: Bougueleret, Lydie  
; TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS  
; FILE REFERENCE: 31. US3.CIP

Query Match 22.8%; Score 52; DB 4; Length 162;  
Best Local Similarity 45.5%; Pred. No. 2.5;  
Matches 10; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 MNGFASILLRNQFILLVFLIQ 22  
DB 24 VNSFSELLQKTPVQLVLFIIQ 45

RESULT 12

US-09-663-600A-220  
; Sequence 220, Application US/09663600A  
; Patent No. 6573068  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste  
; APPLICANT: Duclert, Aymeric  
; APPLICANT: Bougueleret, Lydie  
; TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS  
; FILE REFERENCE: 31.US3.CTP  
; CURRENT APPLICATION NUMBER: US/09/663,600A  
; CURRENT FILING DATE: 2000-09-15  
; PRIOR FILING DATE: 1998-11-13  
; PRIOR APPLICATION NUMBER: 60/066,677  
; PRIOR FILING DATE: 1997-11-13  
; PRIOR APPLICATION NUMBER: 60/069,957  
; PRIOR FILING DATE: 1997-12-17  
; PRIOR APPLICATION NUMBER: 60/074,121  
; PRIOR FILING DATE: 1998-02-09  
; PRIOR APPLICATION NUMBER: 60/081,563  
; PRIOR FILING DATE: 1998-04-13  
; PRIOR APPLICATION NUMBER: 60/096,116  
; PRIOR FILING DATE: 1998-08-10  
; PRIOR APPLICATION NUMBER: 60/099,273  
; PRIOR FILING DATE: 1998-09-04  
; NUMBER OF SEQ ID NOS: 229  
; SOFTWARE: Patent.pm  
; SEQ ID NO 126  
; LENGTH: 162  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SIGNAL  
; LOCATION: -21...-1  
; US-09-663-600A-126

Query Match 22.8%; Score 52; DB 4; Length 162;  
Best Local Similarity 45.5%; Pred. No. 2.5;  
Matches 10; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 MNGFASILLRNQFILLVFLIQ 22  
DB 24 VNSFSELLQKTPVQLVLFIIQ 45

RESULT 12

US-09-663-600A-220  
; Sequence 220, Application US/09663600A  
; Patent No. 6573068  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste  
; APPLICANT: Duclert, Aymeric  
; APPLICANT: Bougueleret, Lydie  
; TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS  
; FILE REFERENCE: 31.US3.CTP  
; CURRENT APPLICATION NUMBER: US/09/663,600A  
; CURRENT FILING DATE: 2000-09-15  
; PRIOR FILING DATE: 1998-11-13  
; PRIOR APPLICATION NUMBER: 60/066,677  
; PRIOR FILING DATE: 1997-11-13  
; PRIOR APPLICATION NUMBER: 60/069,957  
; PRIOR FILING DATE: 1997-12-17  
; PRIOR APPLICATION NUMBER: 60/074,121  
; PRIOR FILING DATE: 1998-02-09  
; PRIOR APPLICATION NUMBER: 60/081,563  
; PRIOR FILING DATE: 1998-04-13  
; PRIOR APPLICATION NUMBER: 60/096,116  
; PRIOR FILING DATE: 1998-08-10  
; PRIOR APPLICATION NUMBER: 60/099,273  
; PRIOR FILING DATE: 1998-09-04  
; NUMBER OF SEQ ID NOS: 229  
; SOFTWARE: Patent.pm  
; SEQ ID NO 220  
; LENGTH: 162  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SIGNAL  
; LOCATION: -94...-1  
; US-09-663-600A-220

Query Match 22.8%; Score 52; DB 4; Length 162;  
Best Local Similarity 45.5%; Pred. No. 2.5;  
Matches 10; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 MNGFASILLRNQFILLVFLIQ 22  
DB 24 VNSFSELLQKTPVQLVLFIIQ 45

RESULT 13

US-09-149-476-462  
; Sequence 462, Application US/09149476  
; Patent No. 8420526  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: 186 Human Secreted proteins  
; FILE REFERENCE: P2002P1  
; CURRENT APPLICATION NUMBER: US/09/149,476  
; CURRENT FILING DATE: 1998-09-08  
; PRIOR APPLICATION NUMBER: PCT/US98/04493  
; EARLIER FILING DATE: 1998-03-06  
; EARLIER APPLICATION NUMBER: 60/040,162  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/040,333  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/038,621  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/040,626  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/040,334  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/040,336  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/040,163  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/047,600  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,615  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,597  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,502  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,633  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,583  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,617  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,618  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,503  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,592  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,581  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,584  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,500  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,587  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,492  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,598  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,613  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,582  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,596  
; EARLIER FILING DATE: 1997-05-23

EARLIER APPLICATION NUMBER: 60/047,612  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,632  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,601  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/043,580  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,568  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,314  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,569  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,311  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,671  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,674  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,669  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,312  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,313  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,672  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,315  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/048,974  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/056,886  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,877  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,889  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,893  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,630  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,878  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,662  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,872  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,882  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,637  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,903  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,888  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,879  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,880  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,894  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,911  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,636  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,874  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,910  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,864  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,631

EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,845  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,892  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/057,761  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/047,595  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,599  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,588  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,585  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,586  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,590  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,594  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,589  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,593  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,614  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/043,578  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,576  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/047,501  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/043,670  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/056,632  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,664  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,876  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,881  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,909  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,875  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,862  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,887  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,908  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/048,964  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/057,650  
EARLIER FILING DATE: 1997-09-05  
EARLIER APPLICATION NUMBER: 60/056,884  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/057,669  
EARLIER FILING DATE: 1997-09-05  
EARLIER APPLICATION NUMBER: 60/049,610  
EARLIER FILING DATE: 1997-06-13  
EARLIER APPLICATION NUMBER: 60/061,060  
EARLIER FILING DATE: 1997-10-02

Query Match 22.8%; Score 52; DB 4; Length 163;  
Best Local Similarity 45.5%; Pred.No. 2.6;  
Matches 10; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 MNGFASLIRNRNOFILLVLFILQ 22  
DB 24 VNSFSELLOKTPVQLVLFILQ 45

RESULT 14  
US-09-252-991A-27295  
; Sequence 27295, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33+42  
; SEQ ID NO 27295  
; LENGTH: 300  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-27295

Query Match 22.6%; Score 51.5; DB 4; Length 300;  
Best Local Similarity 29.3%; Pred. NO. 6.7;  
Matches 17; Conservative 7; Mismatches 15; Indels 19; Gaps 2;  
QY 8 LRNQFLLVLFLLQI-----QSLG---LDIDSRPTAEVCATHITSP 46  
DB 134 LQSMVLLVSVLLQCCRRPPPPRPSGRGQQLGAGEQLDVAADPATVCRDLDP 191

RESULT 15  
US-09-489-039A-13278  
; Sequence 13278, Application US/09489039A  
; Patent No. 6610836  
; GENERAL INFORMATION:  
; APPLICANT: Gary Breton et. al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 2709.2004001  
; CURRENT APPLICATION NUMBER: US/09/489,039A  
; CURRENT FILING DATE: 2000-01-27  
; PRIOR APPLICATION NUMBER: US 60/117,747  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 14342  
; SEQ ID NO 13278  
; LENGTH: 416  
; TYPE: PRT  
; ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-13278

Query Match 21.9%; Score 50; DB 4; Length 416;  
Best Local Similarity 34.3%; Pred. NO. 18;  
Matches 12; Conservative 9; Mismatches 14; Indels 0; Gaps 0;  
QY 1 MNGFASLLRRNQFLLVLFLLQI-----QSLGIDIDSRPT 35  
DB 108 MDYRRVRRLLILLVLLVALLVALLVALLVLLDFMLGPS 142

Search completed: March 8, 2004, 12:17:26  
Job time : 12.9559 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 8, 2004, 11:54:00 ; Search time 42.3524 Seconds

(without alignments)  
306.882 Million cell updates/sec

Title: US-09-600-932-2\_COPY\_1\_46

Perfect score: 228  
Sequence: 1 MNGFASLLRNQFILLVFL.....GLDIDSRPTAEVCATHITSP 46

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A Geneseq 29Jan04:\*

- 1: geneseqp1980a:\*
- 2: geneseqp1990a:\*
- 3: geneseqp2000a:\*
- 4: geneseqp2001a:\*
- 5: geneseqp2002a:\*
- 6: geneseqp2003a:\*
- 7: geneseqp2003bs:\*
- 8: geneseqp2004a:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	228	100.0	277	2	AAY25518 Human col
2	228	100.0	277	2	AAY41698 Human PRO
3	228	100.0	277	3	AAB44254 Human PRO
4	228	100.0	277	4	AU29073 Human PRO
5	228	100.0	277	4	AU58449 Human PRO
6	228	100.0	277	6	ABU87997 Novel hum
7	228	100.0	277	6	ABU84312 Human sec
8	228	100.0	277	6	ABR66186 Human sec
9	228	100.0	277	6	ABR65576 Human sec
10	228	100.0	277	6	ABU99516 Human sec
11	228	100.0	277	6	ABU82755 Human PRO
12	228	100.0	277	6	ABU98976 Novel hum
13	228	100.0	277	6	ABR68125 Human sec
14	228	100.0	277	6	ABU96178 Novel hum
15	228	100.0	277	6	ABU92609 Human sec
16	228	100.0	277	6	ABO08686 Human sec
17	228	100.0	277	6	ABO02738 Human sec
18	228	100.0	277	6	ABR74892 Human sec
19	228	100.0	277	6	ABR94654 Human sec
20	228	100.0	277	6	ABO25200 Novel hum
21	228	100.0	277	6	ABU85627 Novel hum
22	228	100.0	277	6	ABU98787 Novel hum
23	228	100.0	277	6	ABU98002 Novel hum
24	228	100.0	277	6	ABU91708 Novel hum
25	228	100.0	277	6	ABU72206 Novel hum

26	228	100.0	277	6	ABU89401 Human PRO
27	228	100.0	277	6	ABU86242 Human sec
28	228	100.0	277	6	ABU67455 Human PRO
29	228	100.0	277	6	ABU80483 Human PRO
30	228	100.0	277	6	ABR9401 Human sec
31	228	100.0	277	6	ABR98791 Human sec
32	228	100.0	277	6	ABO16314 Human sec
33	228	100.0	277	6	ABR92214 Human sec
34	228	100.0	277	6	ABO18855 Human sec
35	228	100.0	277	6	ABR78276 Human sec
36	228	100.0	277	6	ABU85012 Novel hum
37	228	100.0	277	6	ABO00151 Novel hum
38	228	100.0	277	6	ABO11483 Human sec
39	228	100.0	277	6	ABO02128 Human sec
40	228	100.0	277	6	ABU88702 Human sec
41	228	100.0	277	6	ABU83397 Human sec
42	228	100.0	277	6	ABO06198 Novel hum
43	228	100.0	277	6	ABR59234 Human sec
44	228	100.0	277	6	ABO09296 Human sec
45	228	100.0	277	6	ABO19160 Novel hum

ALIGNMENTS

RESULT 1  
AAY25518  
ID AAY25518 standard; protein; 277 AA.

XX AC AAY25518;  
XX DT 30-SEP-1999 (first entry)  
XX DE Human collectin protein.  
XX KW Collectin; human; antibacterial; antiviral; treatment; infection.  
XX OS Homo sapiens.  
XX PN WO9937767-A1.  
XX PD 29-JUL-1999.  
XX PF 24-JUL-1998; 98WO-JP003328.  
XX PR 23-JAN-1998; 98JP-00011281.  
XX PA (FUSO ) FUSO PHARM IND LTD.  
XX PI Wakamiya N;  
XX DR WPI; 1999-458691/38.  
XX DR N-PSDB; AAX88323.  
XX FT New collectin protein of human origin and DNA encoding it.  
XX PS Claim 1; Page 42-44; 58pp; Japanese.  
XX CC This invention describes the isolation and characterisation of a novel human collectin protein and its encoding polynucleotide. The human collectin exhibits antibacterial and antiviral activity and can be used as an agent for the treatment of human bacterial and viral infections.  
XX CC This sequence represents the novel human collectin

Sequence 277 AA;

Query Match 100.0%; Score 228; DB 2; Length 277;  
Best Local Similarity 100.0%; Pred. No. 4.4e-24;  
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MNGFASLLRNQFILLVFLFLLQSLGLDIDSRPTAEVCATHITSP 46  
DB 1 MNGFASLLRNQFILLVFLFLLQSLGLDIDSRPTAEVCATHITSP 46

RESULT 2  
AA41698  
ID AA41698 standard; protein; 277 AA.  
AC  
XX  
XX  
DT 07-DEC-1999 (first entry)  
XX  
DE Human PRO702 protein sequence.  
XX  
XX Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;  
KW probe; blood coagulation disorder; cancer; cellular adhesion disorder;  
KW secreted protein; transmembrane protein.  
XX  
OS Homo sapiens.  
XX  
XX WO9946281-A2.  
XX  
PD 16-SEP-1999.  
XX  
XX 08-MAR-1999; 99WO-US005028.  
XX  
PR 10-MAR-1998; 98US-0077450P.  
PR 11-MAR-1998; 98US-0077632P.  
PR 11-MAR-1998; 98US-0077641P.  
PR 11-MAR-1998; 98US-0077649P.  
PR 12-MAR-1998; 98US-0077791P.  
PR 13-MAR-1998; 98US-0078004P.  
PR 17-MAR-1998; 98US-0004022P.  
PR 20-MAR-1998; 98US-0078886P.  
PR 20-MAR-1998; 98US-0078910P.  
PR 20-MAR-1998; 98US-0078936P.  
PR 20-MAR-1998; 98US-0078939P.  
PR 25-MAR-1998; 98US-0079294P.  
PR 26-MAR-1998; 98US-0079656P.  
PR 27-MAR-1998; 98US-0079663P.  
PR 27-MAR-1998; 98US-0079664P.  
PR 27-MAR-1998; 98US-0079689P.  
PR 27-MAR-1998; 98US-0079728P.  
PR 27-MAR-1998; 98US-0079786P.  
PR 30-MAR-1998; 98US-0079920P.  
PR 30-MAR-1998; 98US-0079823P.  
PR 31-MAR-1998; 98US-0080103P.  
PR 31-MAR-1998; 98US-0080107P.  
PR 31-MAR-1998; 98US-0080165P.  
PR 31-MAR-1998; 98US-0080194P.  
PR 01-APR-1998; 98US-0080327P.  
PR 01-APR-1998; 98US-0080328P.  
PR 01-APR-1998; 98US-0080333P.  
PR 01-APR-1998; 98US-0080334P.  
PR 08-APR-1998; 98US-0081049P.  
PR 08-APR-1998; 98US-0081070P.  
PR 08-APR-1998; 98US-0081071P.  
PR 09-APR-1998; 98US-0081195P.  
PR 09-APR-1998; 98US-0081203P.  
PR 09-APR-1998; 98US-0081229P.  
PR 15-APR-1998; 98US-0081811P.  
PR 15-APR-1998; 98US-0081838P.  
PR 15-APR-1998; 98US-0081952P.  
PR 15-APR-1998; 98US-0081955P.  
PR 21-APR-1998; 98US-0082568P.  
PR 21-APR-1998; 98US-0082569P.  
PR 22-APR-1998; 98US-0082700P.  
PR 22-APR-1998; 98US-0082704P.  
PR 22-APR-1998; 98US-0082804P.  
PR 23-APR-1998; 98US-0082767P.  
PR 23-APR-1998; 98US-0082796P.  
PR 27-APR-1998; 98US-0083336P.  
PR 28-APR-1998; 98US-0083322P.  
PR 29-APR-1998; 98US-0083392P.  
PR 29-APR-1998; 98US-0083495P.  
PR 29-APR-1998; 98US-0083496P.  
PR 29-APR-1998; 98US-0083497P.  
PR 29-APR-1998; 98US-0083500P.  
PR 29-APR-1998; 98US-0083545P.  
PR 29-APR-1998; 98US-0083554P.  
PR 29-APR-1998; 98US-0083558P.  
PR 29-APR-1998; 98US-0083559P.  
PR 30-APR-1998; 98US-0083742P.  
PR 05-MAY-1998; 98US-0084366P.  
PR 06-MAY-1998; 98US-0084414P.  
PR 06-MAY-1998; 98US-0084441P.  
PR 07-MAY-1998; 98US-0084598P.  
PR 07-MAY-1998; 98US-0084600P.  
PR 07-MAY-1998; 98US-0084627P.  
PR 07-MAY-1998; 98US-0084637P.  
PR 07-MAY-1998; 98US-0084639P.  
PR 07-MAY-1998; 98US-0084840P.  
PR 07-MAY-1998; 98US-0084843P.  
PR 13-MAY-1998; 98US-0085323P.  
PR 13-MAY-1998; 98US-0085338P.  
PR 15-MAY-1998; 98US-0085573P.  
PR 15-MAY-1998; 98US-0085579P.  
PR 15-MAY-1998; 98US-0085580P.  
PR 15-MAY-1998; 98US-0085582P.  
PR 15-MAY-1998; 98US-0085689P.  
PR 15-MAY-1998; 98US-0085697P.  
PR 15-MAY-1998; 98US-0085700P.  
PR 15-MAY-1998; 98US-0085704P.  
PR 18-MAY-1998; 98US-0086023P.  
PR 22-MAY-1998; 98US-0086392P.  
PR 22-MAY-1998; 98US-0086414P.  
PR 22-MAY-1998; 98US-0086430P.  
PR 22-MAY-1998; 98US-0086486P.  
PR 28-MAY-1998; 98US-0087098P.  
PR 28-MAY-1998; 98US-0087106P.  
PR 28-MAY-1998; 98US-0087208P.  
PR 30-JUL-1998; 98US-0094551P.  
PR 11-SEP-1998; 98US-0100038P.  
XX  
XX (GETH ) GENENTECH INC.  
XX  
XX Wood WJ, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;  
PI  
XX  
XX WPI, 1999-551358/46.  
XX N-PSDB; AA333973.  
XX  
XX New secreted and transmembrane polypeptides and their polynucleotides,  
PT useful for treating blood coagulation disorders, cancers and cellular  
PT adhesion disorders.  
XX  
XX Claim 12; Fig 37; 530pp; English.  
XX  
XX The present invention describes secreted and transmembrane polypeptides  
CC and their polynucleotides. The nucleotide sequences are useful as sources  
CC of probes, primers, for chromosome mapping, and for generation of  
CC antisense sequences. They can also be used to create transgenic animals.  
CC The proteins can be used to treat a variety of diseases and disorders,  
CC depending on their function. Diseases that may be treated include blood  
CC coagulation disorders, cancers and cellular adhesion disorders. They may  
CC also be used to raise antibodies. AA333891 to AA334338, and AA41685 to  
CC AA41774 represent polynucleotide and polypeptide sequence given in the  
CC exemplification of the present invention  
XX  
XX Sequence 277 AA;  
SQ  
Query Match 100.0%; Score 228; DB 2; Length 277;  
Best Local Similarity 100.0%; Pred. No. 4.4e-24;  
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MNGFASLRNRNQFILLVFLFIQSLGLDIDSRPTAEVCATHITSP 46  
DB 1 MNGFASLRNRNQFILLVFLFIQSLGLDIDSRPTAEVCATHITSP 46



## RESULT 3

ID AAB44254 standard; protein; 277 AA.

XX AAB44254;  
AC AAB44254;

DT 08-FEB-2001 (first entry)

DE Human PRO702 (UNQ366) protein sequence SEQ ID NO:97.

KW Human; secreted protein; transmembrane protein; PRO; EST; cytostatic;  
KW expressed sequence tag; detection; cancer.

XX Homo sapiens.

XX WO200053756-A2.

XX 14-SEP-2000.

XX 18-FEB-2000; 2000WO-US004341.

XX 08-MAR-1999; 99WO-US005028.

XX 12-MAR-1999; 99US-0123957P.

XX 29-MAR-1999; 99US-0126773P.

XX 21-APR-1999; 99US-0130232P.

XX 28-APR-1999; 99US-0131445P.

XX 14-MAY-1999; 99US-0134287P.

XX 23-JUN-1999; 99US-0141037P.

XX 26-JUL-1999; 99US-0145698P.

XX 29-OCT-1999; 99US-0162506P.

XX 02-DEC-1999; 99WO-US028313.

XX 02-DEC-1999; 99WO-US028551.

XX 16-DEC-1999; 99WO-US028565.

XX 30-DEC-1999; 99WO-US030035.

XX 30-DEC-1999; 99WO-US031243.

XX 05-JAN-2000; 99WO-US031274.

XX 06-JAN-2000; 2000WO-US000219.

XX 06-JAN-2000; 2000WO-US000277.

XX 06-JAN-2000; 2000WO-US000376.

XX (GETH ) GENENTECH INC.

XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
XX Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;  
XX Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;  
XX Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;  
XX Stewart TA, Tumas D, Williams PM, Wood WI;

XX WPI; 2000-611443/58.

XX N-PSDB; AAC78480.

XX Novel PRO polypeptides and polynucleotides used in detection methods, to  
XX target bioactive molecules to specific cells, and to modulate cellular  
XX activities.

XX Claim 12; Fig 37; 636pp; English.

XX AAC78458 to AAC78599 represent polynucleotide and EST (expressed sequence  
XX tag) sequences which encode secreted or transmembrane PRO polypeptides.  
XX The PRO polynucleotides and polypeptides have cytostatic activity. The  
XX polynucleotides and polypeptides can be used for detecting the presence  
XX of PRO polypeptides in samples, for linking bioactive molecules to cells  
XX and for modulating biological activities of cells, using the polypeptides  
XX for specific targeting. The polypeptide targeting can be used to kill the  
XX target cells, e.g. for the treatment of cancers. The polypeptide pairs  
XX provide specific targeting of bioactive molecules to cells. AAC78600 to  
XX AAC78987 represent PCR primers and probes used in the isolation of the  
XX PRO polynucleotide sequences

XX Sequence 277 AA;

SQ

Query Match 100.0%; Score 228; DB 3; Length 277;  
Best Local Similarity 100.0%; Pred. NO. 4.4e-24;  
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;QY 1 MNGFASLLRRNQFILLVLFLLQIQSLGLDIDSRPTAEVCATHTISP 46  
DB 1 MNGFASLLRRNQFILLVLFLLQIQSLGLDIDSRPTAEVCATHTISP 46

## RESULT 4

ID AAU29073 standard; protein; 277 AA.

XX AAU29073;  
AC AAU29073;

DT 18-DEC-2001 (first entry)

DE Human PRO polypeptide sequence #50.

KW PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;  
KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;  
KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;  
KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.

XX Homo sapiens.

XX WO200168848-A2.

XX 20-SEP-2001.

XX 28-FEB-2001; 2001WO-US006520.

XX 01-MAR-2000; 2000WO-US005601.

XX 02-MAR-2000; 2000WO-US005841.

XX 03-MAR-2000; 2000US-0187202P.

XX 06-MAR-2000; 2000US-0186968P.

XX 14-MAR-2000; 2000US-0189320P.

XX 14-MAR-2000; 2000US-0189328P.

XX 15-MAR-2000; 2000WO-US006884.

XX 21-MAR-2000; 2000US-0190828P.

XX 21-MAR-2000; 2000US-0191007P.

XX 21-MAR-2000; 2000US-0191048P.

XX 21-MAR-2000; 2000US-0191314P.

XX 28-MAR-2000; 2000US-0192655P.

XX 29-MAR-2000; 2000US-0193032P.

XX 29-MAR-2000; 2000US-0193053P.

XX 30-MAR-2000; 2000WO-US008439.

XX 04-APR-2000; 2000US-0194449P.

XX 04-APR-2000; 2000US-0194647P.

XX 11-APR-2000; 2000US-0195375P.

XX 11-APR-2000; 2000US-0196000P.

XX 11-APR-2000; 2000US-0196187P.

XX 11-APR-2000; 2000US-0196690P.

XX 18-APR-2000; 2000US-0198121P.

XX 18-APR-2000; 2000US-0198585P.

XX 25-APR-2000; 2000US-0199397P.

XX 25-APR-2000; 2000US-0199550P.

XX 03-MAY-2000; 2000US-0201516P.

XX 17-MAY-2000; 2000WO-US013705.

XX 22-MAY-2000; 2000WO-US014042.

XX 30-MAY-2000; 2000WO-US014941.

XX 02-JUN-2000; 2000WO-US015264.

XX 05-JUN-2000; 2000US-0209832P.

XX 28-JUL-2000; 2000WO-US020710.

XX 22-AUG-2000; 2000US-00644848.

XX 24-AUG-2000; 2000WO-US023328.

XX 08-NOV-2000; 2000WO-US030952.

XX 01-DEC-2000; 2000WO-US032678.

XX 20-DEC-2000; 2000WO-US034956.

XX (GETH ) GENENTECH INC.

XI Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;  
 PI Pan J, Smith V, Watanabe CK, Wood WL, Zhang Z;  
 XX WPI; 2001-602746/68.  
 DR N-PSDB; AAS45974.  
 XX Novel nucleic acids encoding PRO polypeptides, used to diagnose the  
 PT presence of tumors, such as prostate and breast tumors, in mammals and to  
 PT screen for modulators of the compounds.  
 XX Claim 11; Fig 100; 774pp; English.  
 XX Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.  
 CC The PRO polypeptides and their associated nucleic acids can be used to  
 CC detect the presence of a tumour in a mammal by comparing the level of  
 CC expression of a PRO polypeptide in a test sample of cells from the animal  
 CC and a control sample of normal cells, whereby a higher level of  
 CC expression in the test sample indicates the presence of a tumour in the  
 CC mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats  
 CC and rabbits but are preferably human. The polypeptides can be used to  
 CC stimulate tumour necrosis factor (TNF) alpha release from human blood,  
 CC when contacted with it. A specific polypeptide can be used to stimulate  
 CC the proliferation or differentiation of chondrocyte cells. The PRO  
 CC proteins can be used to determine the presence of tumours and also  
 CC susceptibility to tumour development, particularly adrenal, lung, colon,  
 CC breast, prostate, rectal, cervical, or liver tumours, in mammalian  
 CC subjects. The oligonucleotide probes specific for the PRO nucleic acids  
 CC can be used for genetic analysis of individuals with genetic disorders  
 XX Sequence 277 AA;  
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 Best Local Similarity 100.0%; Pred. No. 4.4e-24;  
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 AC ABUS8449;  
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 DE Human; PRO; cytostatic; tumour; cancer; breast; lung; stomach; liver;  
 KW dog; cat; cow; horse; sheep; pig; goat; rabbit; ADEPT;  
 KW antibody-dependent enzyme mediated prodrug therapy.  
 XX Homo sapiens.  
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XX ABUS7997;

XX AC

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XX 07-JUL-2003 (first entry)

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XX Novel human secreted and transmembrane protein PRO702.

XX KW Human; secreted and transmembrane protein; PRO; gene therapy;  
tumour necrosis factor-alpha release; TNF-alpha release;  
chondrocyte proliferation; chondrocyte differentiation; tumour;  
adrenal tumour; lung tumour; colon tumour; breast tumour;  
prostate tumour; rectal tumour; cervical tumour; liver tumour.

XX KW

XX OS Homo sapiens.

XX OS

XX US2003032127-A1.

XX PN

XX 13-FEB-2003.

XX PD

XX 26-JUN-2002; 2002US-00183012.

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XX DT 02-AUG-2003 (first entry)
XX DE Human secreted/transmembrane protein (PRO) #50.
XX KW Human; secreted and transmembrane protein; PRO; TNF-alpha;
XX KW Tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
XX OS Homo sapiens.
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XX KW Human; PRO; secreted protein; transmembrane protein; TNF-alpha;  
KW extracellular domain; tumour necrosis factor-alpha; TNF-alpha;  
KW chondrocyte; proliferation; differentiation; cartilage disorder;  
KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;  
KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;  
KW liver; drug screening; transgenic animal; genetic analysis;  
KW antiarthritic; vulnery; gene therapy.  
XX OS Homo sapiens.  
XX SS US2003027278-A1.  
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XX DE Human secreted polypeptide PRO702, SEQ ID NO:100.
XX KW Human; PRO; secreted protein; transmembrane protein;
XX KW extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
XX KW chondrocyte; proliferation; differentiation; cartilage disorder;
XX KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
XX KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
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DB 1 MNGFASLLRNNQFILLVLFLLQIQSLGLDIDSRPTAECATHTISP 46

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XX AC ABU99516;
XX DT 09-AUG-2003 (first entry)
XX DE Human secreted/transmembrane protein (PRO) #50.
XX KW Human; secreted and transmembrane protein; PRO; TNF-alpha;
KW tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
XX tissue typing.
XX OS Homo sapiens.
XX PN US2003040070-A1.
XX PD 27-FEB-2003.
XX PF 27-JUN-2002; 2002US-00184627.
XX PR 18-SEP-1997; 97US-0059263P.
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Db 1 MNGFASLLRRNFILVFLFLLQISGLDIDSRPTAEVCATHITSP 46

RESULT 12  
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ID ABUS9876 standard; protein; 277 AA.  
XX  
AC ABUS9876;  
XX  
DT 11-AUG-2003 (first entry)  
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DE Novel human secreted and transmembrane protein PRO702.  
XX Human; gene therapy; tissue typing; tumour; chondrocyte proliferation;  
KW chondrocyte differentiation; tumour necrosis factor-alpha release;  
KW affinity purification.  
XX Homo sapiens.  
OS US2003036147-A1.  
PN 20-FEB-2003.  
XX  
PD 02-JUL-2002; 2002US-00187741.  
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KW liver; drug screening; transgenic animal; genetic analysis;  
XX antiarthritic; vulnerary; gene therapy.

OS Homo sapiens.

PN US2003027264-A1.

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XX 06-FEB-2003.

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GenCore version 5.1.6  
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; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
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; FILE REFERENCE: P2630P1C11  
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; PRIOR APPLICATION NUMBER: 09/918585

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; PRIOR APPLICATION NUMBER: 60/085697

Query Match          99.0%; Score 390; DB 9; Length 277;
Best Local Similarity 98.6%; Pred. No. 5.8e-34;
Matches 71; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 61 GIPGKGKAGTV 72
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RESULT 2
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; Sequence 97, Application US/09978697
; Patent No. US20020169284A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630FIC27
; CURRENT APPLICATION NUMBER: US/09/978,697
; CURRENT FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
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Best Local Similarity 98.6%; Pred. No. 5.8e-34;  
Matches 71; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
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; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnovers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
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; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
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; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2630P1C9  
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; PRIOR FILING DATE: 1997-11-03  
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63	PRIOR APPLICATION NUMBER: 60/085338
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66	PRIOR FILING DATE: 1998-05-13
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68	PRIOR FILING DATE: 1998-05-15
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Query Match 99.0%; Score 390; DB 9; Length 277;

Best Local Similarity 98.6%; Pred. No. 5.8e-34;

Matches 71; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 4

US-09-999-832A-97

; Sequence 97, Application US/09999832A

; Publication No. US20020192706A1

GENERAL INFORMATION:

APPLICANT: Aehkenazi, Avi

APPLICANT: Baker Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan

APPLICANT: Ferrara, Napoleon

APPLICANT: Filvaroff, Ellen

APPLICANT: Fong, Sherman

APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.

APPLICANT: Hillan, Kenneth J.

APPLICANT: Kijavlin, Ivar J.

APPLICANT: Kuo, Sophia S.

APPLICANT: Napier, Mary A.

APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Shelton, David L.

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

FILE REFERENCE: F2630PIC63

CURRENT APPLICATION NUMBER: US/09/999,832A

CURRENT FILING DATE: 2001-10-24

PRIOR APPLICATION NUMBER: 09/918585

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;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 99.0%; Score 390; DB 9; Length 277;  
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Matches 71; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPKGDDGKGDGEGKHGKVGWGPKGIGKELGDMGDRGNICKTGPIGKGGKGEKGLL 60  
Db 47 GPKGDDGKGDGEGKHGKVGWGPKGIGKELGDMGDRGNICKTGPIGKGGKGEKGLL 106  
QY 61 GIPGEGKAGTV 72  
Db 107 GIPGEGKAGTV 118

## RESULT 5

US-09-978-189-97  
; Sequence 97, Application US/09978189  
; Publication No. US20030004102A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Paoli, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2630P1C7  
; CURRENT APPLICATION NUMBER: US/09/978,189  
; CURRENT FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: 09/918585  
; PRIOR FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: 60/082250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/064249  
; PRIOR FILING DATE: 1997-11-03  
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; PRIOR FILING DATE: 1998-03-10  
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match
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Db 47 GPKGDDGKGPGEKGKGVGRMGPKIGKELGMDGDRNIGKTGPIGKKGDKGKGLL 106

2Y 61 GIPGEKKGAGTV 72
Db 107 GIPGEKKGAGTV 118

RESULT 6
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; Publication No. US20030045462A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C22
; CURRENT APPLICATION NUMBER: US/09/978,608A
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 97
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US-09-978-608A-97

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Matches 71; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db 47 GPKGDDGKGPGEKGKGVGRMGPKIGKELGMDGDRNIGKTGPIGKKGDKGKGLL 106

2Y 61 GIPGEKKGAGTV 72
Db 107 GIPGEKKGAGTV 118

RESULT 7
US-09-978-585A-97
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; Publication No. US20030049633A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
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; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
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; APPLICANT: Kuo, Sophia S.
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; APPLICANT: Roy, Margaret Ann
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; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C15
; CURRENT APPLICATION NUMBER: US/09/978,585A
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
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US-09-978-585A-97

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Db 107 GIPGEKKGAGTV 118

RESULT 8
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; Publication No. US20030050239A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan
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; GENERAL INFORMATION:
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; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan
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; APPLICANT: Filvaroff, Ellen
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; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
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US-09-978-585A-97

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Db 107 GIPGEKKGAGTV 118

RESULT 8
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APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
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FILE REFERENCE: P2630P1C4  
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CURRENT FILING DATE: 2001-10-15  
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;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 99.0%; Score 390; DB 10; Length 277;

Best Local Similarity 98.6%; Pred. No. 5.8e-34;

Matches 71; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPKGDDGKGPGEKGKGVGRMGPKIGKGLGMDGRNGTKGTGPKGKGDKGKGLL 60

Db 47 GPKGDDGKGPGEKGKGVGRMGPKIGKGLGMDGQGNIGTKGTGPKGKGDKGKGLL 106

QY 61 GIPGKKGKAGTV 72

Db 107 GIPGKKGKAGTV 118

# RESULT 9

US-09-978-403A-97

; Sequence 97, Application US/09978403A

; Publication No. US2003005240A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleon

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

;; APPLICANT: Gao, Wei-Qiang  
;; APPLICANT: Gerber, Hanspeter  
;; APPLICANT: Gerritsen, Mary E.  
;; APPLICANT: Goddard, Audrey  
;; APPLICANT: Godowski, Paul J.  
;; APPLICANT: Grimaldi, J. Christopher  
;; APPLICANT: Gurney, Austin L.  
;; APPLICANT: Hillan, Kenneth J.  
;; APPLICANT: Kljavin, Ivar J.  
;; APPLICANT: Kuo, Sophia S.  
;; APPLICANT: Napier, Mary A.  
;; APPLICANT: Pan, James  
;; APPLICANT: Paoni, Nicholas F.  
;; APPLICANT: Roy, Margaret Ann  
;; APPLICANT: Shelton, David L.  
;; APPLICANT: Stewart, Timothy A.  
;; APPLICANT: Tunas, Daniel  
;; APPLICANT: Williams, P. Mickey  
;; APPLICANT: Wood, William I.  
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
;; FILE REFERENCE: P2630P1C17  
;; CURRENT APPLICATION NUMBER: US/09/978,403A  
;; CURRENT FILING DATE: 2002-03-19  
;; PRIOR APPLICATION NUMBER: 09/918585  
;; PRIOR FILING DATE: 2001-07-30  
;; PRIOR APPLICATION NUMBER: 60/062250  
;; PRIOR FILING DATE: 1997-10-17  
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;; PRIOR FILING DATE: 1998-03-30  
;; PRIOR APPLICATION NUMBER: 60/079923  
;; PRIOR FILING DATE: 1998-03-30  
;; PRIOR APPLICATION NUMBER: 60/080105



APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2630P1C25  
CURRENT APPLICATION NUMBER: US/09/978,564A  
CURRENT FILING DATE: 2001-10-16  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
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PRIOR FILING DATE: 1997-10-17  
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PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080327  
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 ; PRIOR FILING DATE: 1998-05-15  
 ; PRIOR APPLICATION NUMBER: 60/085697

Query Match 99.0%; Score 390; DB 10; Length 277;  
 Best Local Similarity 98.6%; Pred. No. 5.8e-34;  
 Matches 71; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GPKGDDGKGDGPKGKGVGRGPKGKGLDMDGRNIGKTGPIGKKGKGGKGLL 60  
 Db 47 GPKGDDGKGDGPKGKGVGRGPKGKGLDMDGQNGNIGKTGPIGKKGKGGKGLL 106  
 QY 61 GIPGKGRAGTV 72  
 Db 107 GIPGKGRAGTV 118

RESULT 11  
 US-09-999-833A-37  
 ; Sequence 97, Application US/09999833A  
 ; Publication No. US20030054405A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ashkenazi, Avi  
 ; APPLICANT: Baker Kevin P.  
 ; APPLICANT: Botstein, David  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Eaton, Dan  
 ; APPLICANT: Ferrara, Napoleon  
 ; APPLICANT: Filvaroff, Ellen  
 ; APPLICANT: Fong, Sherman  
 ; APPLICANT: Gao, Wei-Qiang  
 ; APPLICANT: Gerber, Hanspeter  
 ; APPLICANT: Gerritsen, Mary E.  
 ; APPLICANT: Goddard, Audrey  
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; APPLICANT: Gurney, Austin L.  
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 ; APPLICANT: Shelton, David L.  
 ; APPLICANT: Stewart, Timothy A.  
 ; APPLICANT: Tumas, Daniel  
 ; APPLICANT: Williams, P. Mickey  
 ; APPLICANT: Wood, William I.  
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 ; FILE REFERENCE: P2630P1C65  
 ; CURRENT APPLICATION NUMBER: US/09/999,833A  
 ; CURRENT FILING DATE: 2001-10-24  
 ; PRIOR APPLICATION NUMBER: 09/918585  
 ; PRIOR FILING DATE: 2001-07-30  
 ; PRIOR APPLICATION NUMBER: 60/062250  
 ; PRIOR FILING DATE: 1997-10-17  
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; PRIOR FILING DATE: 1998-03-31  
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; PRIOR FILING DATE: 1998-04-01  
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; PRIOR APPLICATION NUMBER: 60/085704  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 99.0%; Score 390; DB 10; Length 277;

Best Local Similarity 98.6%; Pred. No. 5.8e-34;

Matches 71; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPKGDDGKGDGFGKGGKGVGMGPKGKGLGDMGDRGNIGKTGPIGKKGDKGKGLL 60

Db 47 GPKGDDGKGDGFGKGGKGVGMGPKGKGLGDMGDRGNIGKTGPIGKKGDKGKGLL 106

Qy 61 GIPGKKGKAGTV 72

Db 107 GIPGKKGKAGTV 118

RESULT 12

US-09-981-915A-97

; Sequence 97, Application US/09981915A

; Publication No. US20030054986A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Baker Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleon

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Kljavin, Ivar J.

APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James;  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2630P1C12  
CURRENT APPLICATION NUMBER: US/09/981,915A  
PRIOR FILING DATE: 2001-10-16  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
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PRIOR APPLICATION NUMBER: 60/084414  
PRIOR FILING DATE: 1998-05-06  
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66	PRIOR APPLICATION NUMBER: 60/083742
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3	PRIOR APPLICATION NUMBER: 60/084598
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31	PRIOR APPLICATION NUMBER: 60/085697

Query Match 99.0%; Score 390; DB 10; Length 277;

	Best Local Similarity	98.6%;	Pred. No. 5.8e-34;	Mismatches	0;	Indels	0;	Gaps	0;
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106 106

61 GIPGEKGAGTV 72  
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Db 107 GIPGEKGKAGTV 118

RESIT.T 14

RESULT 14  
US-09-918-585A-97

US-09-518-385A-3)  
: Sequence 97. Application US/09918585A

Sequence 37, Application 03/0333  
Publication No. US20030060406A1

; PUBLICATION NO. US20  
; GENERAL INFORMATION:  
; GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi

APPLICANT: ABDUKENAZI, AVI  
APPLICANT: Baker Kevin P.

APPLICANT: BAKER, KEVIN F.  
APPLICANT: BOTSTEIN, DAVID

APPLICANT: BOLSCHEV, DAVID  
APPLICANT: Desnoyers, Luc

APPLICANT: Destroyers, Dan  
APPLICANT: Eaton, Dan

APPLICANT: Ferrara, Napoleon

APPLICANT: Ferrara, Napoleone  
APPLICANT: Filvaroff, Elie

APPLICANT: Fong, Sherman

APPLICANT: FONG, Sherman  
APPLICANT: GAO, Wei-Qiang

APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.

APPLICANT: Gerritsen, Mary

APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul

APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney Austin L.

APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan Kenneth J.

APPLICANT: Hillan, Kenneth  
APPLICANT: Klijian, Tavar J

APPLICANT: KLJAVIN, Ivar J

APPLICANT: Kuo, Sophia S.  
APPLICANT: Natter, Mary A.

APPLICANT: Napier, Mary

; APPLICANT: Pan, James;  
; APPLICANT: Pan, James;  
; APPLICANT: Pan, James;

APPLICANT: Paoni, Nicholas F  
 DOB: 03/03/1974

APPLICANT: Roy, Margaret Ann

APPLICANT: Stewart, Timothy A.  
APPLICANT: Tamas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2630P1C1  
CURRENT APPLICATION NUMBER: US/09/918,585A  
CURRENT FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
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PRIOR APPLICATION NUMBER: 60/084640  
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PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/086023

Query Match 99.0%; Score 390; DB 10; Length 277;  
Best Local Similarity 98.6%; Pred. No. 5.8e-34;  
Matches 71; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
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Db 47 GPKGDGEKGDPEEGKHGKVGMPGKIGKELGMDGRNIGTKGPIGKKGDKGKGLL 106  
Qy 61 GIPGEGKAGTV 72  
Db 107 GIPGEGKAGTV 118

RESULT 15  
US-09-978-423A-97  
Sequence 97 Application US/09978423A  
Publication No. US20030069178A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Deenoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Flivaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
Acids Encoding the Same  
FILE REFERENCE: P2630P1C21  
CURRENT APPLICATION NUMBER: US/09/978,423A  
CURRENT FILING DATE: 2002-05-16  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
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PRIOR FILING DATE: 1998-04-01  
PRIOR APPLICATION NUMBER: 60/080334  
PRIOR FILING DATE: 1998-04-01  
PRIOR APPLICATION NUMBER: 60/081070  
PRIOR FILING DATE: 1998-04-08  
PRIOR APPLICATION NUMBER: 60/081049

Search completed: March 8, 2004, 12:18:56  
Job time : 26.0088 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 8, 2004, 12:02:31 ; Search time 55.1894 Seconds  
(without alignments)  
411.624 Million cell updates/sec

Title: US-09-600-932-2\_COPY\_47\_118

Perfect score: 394

Sequence: 1 GPKGDDGKGDPGEGKHGK.....DKGKGLGIPGKKGATV 72

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SPRENBL\_25.\*

- 1: sp\_archaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_mhc.\*
- 8: sp\_organelle.\*
- 9: sp\_phage.\*
- 10: sp\_plant.\*
- 11: sp\_rodent.\*
- 12: sp\_virus.\*
- 13: sp\_vertebrate.\*
- 14: sp\_unclassified.\*
- 15: sp\_virus.\*
- 16: sp\_bacteriopl.\*
- 17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	394	100.0	277	4	Q9Y6Z7
2	351	89.1	277	11	Q8CF98
3	351	89.1	277	11	Q8C1C5
4	207	52.5	268	2	Q9F685
5	205	52.0	645	2	Q9KXB9
6	205	52.0	645	9	Q9XJK8
7	205	52.0	645	9	Q7V3C2
8	205	52.0	645	9	Q72W1
9	205	52.0	645	16	Q8XAX7
10	205	52.0	678	9	Q8SCA4
11	196	49.7	1723	5	Q9GQB1
12	195.5	49.6	465	2	Q9AGC4
13	195	49.5	465	12	Q8QTH5
14	194	49.2	271	4	Q9EMF8
15	193.5	49.1	291	2	Q9F690
16	193	49.0	688	11	Q9K2W0

17	193	49.0	688	11	Q07643
18	192	48.7	272	11	Q9DC75
19	191	48.5	271	13	Q7T0T0
20	190.5	48.4	410	2	Q9F691
21	189	48.0	397	2	Q9F686
22	186.5	47.3	1779	5	Q9VMV4
23	185	47.0	396	2	Q9AGC5
24	184.5	46.8	344	9	Q857L6
25	184.5	46.8	1366	4	Q15177
26	184.5	46.8	1366	4	Q7Z5S6
27	184.5	46.8	2551	16	Q8CYI8
28	184	46.7	380	2	Q9F692
29	184	46.7	400	2	Q9F689
30	183.5	46.6	291	5	Q23422
31	183.5	46.6	434	2	Q9ACN4
32	183	46.4	1349	13	Q8AW17
33	182	46.2	285	16	Q832X8
34	182	46.2	1549	11	Q60444
35	182	46.2	1714	4	Q7Z5L5
36	182	46.2	1827	13	Q8UUM5
37	181.5	46.1	1439	5	Q97406
38	181	45.9	690	13	Q8JGL8
39	181	45.9	1684	12	Q8VAA1
40	181	45.9	1684	12	Q8JNB6
41	181	45.9	1684	12	Q91LK9
42	180.5	45.8	660	5	Q86D04
43	180	45.7	181	9	Q9ZXF4
44	180	45.7	444	2	Q8RLX7
45	180	45.7	708	13	Q7ZWN8

#### ALIGNMENTS

#### RESULT 1

Q9Y6Z7 PRELIMINARY; PRT; 277 AA.  
 AC Q9Y6Z7; (TRENBLrel. 12, Created)  
 DT 01-NOV-1999 (TRENBLrel. 12, Last sequence update)  
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)  
 DE Collectin 34.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99240768; PubMed=10224141;  
 RA Ohtani K., Suzuki Y., Bda S., Kawai T., Kase T., Yamazaki H.,  
 RA Keshi H., Sakai Y., Fukuh A., Sakamoto T., Wakamiya N.,  
 RT "Molecular cloning of a novel collectin from liver (CL-L1).";  
 RL J. Biol. Chem. 274:13681-13689 (1999).  
 DR EMBL; AB002631; BAA81747.1; -.  
 DR HSSP; P19999; 2MSB.  
 DR Genew; HGNC:2220; COLEC10.  
 DR GO; GO:0005737; C:cytoplasm; TAS.  
 DR GO; GO:0005530; F:lectin; TAS.  
 DR InterPro; IPR008160; Collagen.  
 DR InterPro; IPR001304; LECTIN\_C.  
 DR Pfam; PF01391; Collagen; 1.  
 DR Pfam; PF00059; lectin\_c; 1.  
 DR SMART; SM00034; CLECT; 1.  
 DR PROSITE; PS00615; C-TYPE LECTIN\_1; 1.  
 DR PROSITE; PS50041; C-TYPE LECTIN\_2; 1.  
 SQ SEQUENCE 277 AA; 30733 MW; 9736861CEBDC525 CRC64;

Query Match 100.0%; Score 394; DB 4; Length 277;  
 Best Local Similarity 100.0%; Pred. No. 5.1e-34;  
 Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPKGDDGKGDPGEGKHGKVGKGLGMDGRNIGTKPIGKKGKSGKLL 60



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Db 47 GPKGDDDEKDPGEKGKGVGMGPKGIGKLGMDGRGNIGKTGPIGKKGDKGKGLL 106
QY 61 GIPGEKGKAGTV 72
    |||||
Db 107 GIPGEKGKAGTV 118

RESULT 2
ID Q8CF98 PRELIMINARY; PRT; 277 AA.
AC Q8CF98;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Collectin-L1. (Mouse).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RX MEDLINE=22333927; PubMed=12450124;
RA Kawai T., Suzuki Y., Eda S., Kase T., Ohtani K., Sakai Y., Keshi H.,
RA Fukuchi A., Sakamoto T., Nozaki M., Copeland N.G., Jenkins N.A.,
RA Wakamiya N.;
RT "Molecular Cloning of Mouse Collectin Liver 1.";
RL Biosci. Biotechnol. Biochem. 66:2134-2145(2002).
DR EMBL; AB018429; BAC53954.1; -.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR008160; Collagen.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF01391; Collagen; 1.
DR Pfam; PF00059; lectin c; 1.
DR SMART; SM00034; CLECT_1.
DR PROSITE; PS00615; C-TYPE_LECTIN_1; 1.
DR PROSITE; PS0041; C-TYPE_LECTIN_2; 1.
DR NCBI_TaxID=10090;
RP SEQUENCE 277 AA; 30524 MW; 58C743A2E07A2872 CRC64;

Query Match 89.1%; Score 351; DB 11; Length 277;
Best Local Similarity 87.5%; Pred. No. 1.9e-29;
Matches 63; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 GPKGDDDEKDPGEKGKGVGMGPKGIGKLGMDGRGNIGKTGPIGKKGDKGKGLL 60
Db 47 GPKGDDDEKDPGEKGKGVGMGPKGIGKLGMDGRGNIGKTGPIGKKGDKGKGLL 106

QY 61 GIPGEKGKAGTV 72
    |||||
Db 107 GIPGEKGKAGTV 118

RESULT 3
ID Q8C1C5 PRELIMINARY; PRT; 277 AA.
AC Q8C1C5;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Collectin 34 homolog.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
```

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DR EMBL; AK028423; BAC25941.1; -.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR008160; Collagen.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF01391; Collagen; 1.
DR Pfam; PF00059; lectin c; 1.
DR SMART; SM00034; CLECT_1.
DR PROSITE; PS00615; C-TYPE_LECTIN_1; 1.
DR PROSITE; PS0041; C-TYPE_LECTIN_2; 1.
DR NCBI_TaxID=10090;
RP SEQUENCE 277 AA; 30510 MW; 94EF23A2E5404872 CRC64;

Query Match 89.1%; Score 351; DB 11; Length 277;
Best Local Similarity 87.5%; Pred. No. 1.9e-29;
Matches 63; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 GPKGDDDEKDPGEKGKGVGMGPKGIGKLGMDGRGNIGKTGPIGKKGDKGKGLL 60
Db 47 GPKGDDDEKDPGEKGKGVGMGPKGIGKLGMDGRGNIGKTGPIGKKGDKGKGLL 106

QY 61 GIPGEKGKAGTV 72
    |||||
Db 107 GIPGEKGKAGTV 118

RESULT 4
ID Q9F685 PRELIMINARY; PRT; 268 AA.
AC Q9F685;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-JUN-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Collagen-like surface protein (Fragment).
DE Streptococcus pyogenes.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AP55;
RX MEDLINE=20490571; PubMed=11035747;
RA Rasmussen M., Eden A., Bjorck L.;
RT "ScIA, a novel collagen-like surface protein of streptococcus
RT pyogenes.";
RL Infect. Immun. 68:6370-6377(2000).
DR EMBL; AF298338; AAC30218.1; -.
DR InterPro; IPR008160; Collagen.
DR Pfam; PF01391; Collagen; 1.
DR FT NON TER 1
DR FT NON TER 268
DR NCBI_TaxID=1314;
RP SEQUENCE 268 AA; 28668 MW; 2B42FBA768BC6663 CRC64;

Query Match 52.5%; Score 207; DB 2; Length 268;
Best Local Similarity 64.1%; Pred. No. 3.6e-14;
Matches 41; Conservative 3; Mismatches 20; Indels 0; Gaps 0;

QY 7 GEKGDPPGEKGKGVGMGPKGIGKLGMDGRGNIGKTGPIGKKGDKGKGLLGPGEK 66
Db 109 GEKGDPPGEKGKGVGMGPKGIGKLGMDGRGNIGKTGPIGKKGDKGKGLLGPGEK 168

QY 67 GKAG 70
    |||
Db 169 GPAG 172

RESULT 5
ID Q9KX89 PRELIMINARY; PRT; 645 AA.
AC Q9KX89;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Tail fiber protein.
DE H0137.
```



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EMBL; AE005298; AAC55604.1; -.
EMBL; AF002554; BAB34651.1; -.
PIR; D90782; D90782.
PIR; H85642; H85642.
InterPro; IPR008969; Carboxypeptid_reg.
InterPro; IPR008161; Clg_helix.
InterPro; IPR008161; Collagen.
InterPro; IPR005068; Phage_fiber_2.
Pfam; PF01391; Collagen; 4_fiber_2.
Pfam; PF03406; Phage_fiber_2; 1.
ProDom; PD000007; Clg_helix; 2.
Complete proteome.
SEQUENCE 645 AA; 63955 MW; DE360743A572FF4A CRC64;

Query Match          52.0%; Score 205; DB 16; Length 645;
Best Local Similarity 54.3%; Pred.No.1.7e-13;
Matches 38; Conservative 11; Mismatches 21; Indels 0; Gaps 0;

QY      1  GPKGDGDEKDPDPEEGKHGVGRMPKGIGKELGDMGDGRGNIGKTGPIGKKDKGEKGLL 60
DBb     |||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
247  GPQGSETPGKDVGVPKGKETPVGPQQGAPGPKGERGVGAAGVAPGPRGKEGQERGFQ 306

QY      61  GPIGEKGKAG 70
DBb     |||::|||

307  GIPLKGDGTG 316

RESULT 10
Q8SCA4 Q8SCA4 PRELIMINARY; PRT; 678 AA.
IID Q8SCA4 AC
AC Q8SCA4;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
DE Stx2 converting bacteriophage T.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
OC Lambda-like viruses.
OC NCBI_TaxID=180816;
OX RN [1]
RN SEQUENCE FROM N.A.
STRAIN=Stx2 phage-T;
RC Sato T., Shimizu T., Watarai M., Kobayashi M., Kano S., Hamabata T.,
RA Yanasaki S., Takeda Y.;
RA "Genomic sequence of Shiga toxin 2-converting phage isolated from
RT Escherichia coli O157:H7 Okayama strain and comparison with other
RT Shiga toxin 2-converting phages."
RL Submitted (DEC-2001) to the EMBL/GenBank/DDJ databases.
EMBL; AP004402; BAB87868.1; -.
DR InterPro; IPR008969; Carboxypeptid_reg.
DR InterPro; IPR008161; Clg_helix.
DR InterPro; IPR008160; Collagen.
DR InterPro; IPR005068; Phage_fiber_2.
DR Pfam; PF01391; Collagen; 5.
DR Pfam; PF03406; Phage_fiber_2; 1.
DR ProDom; PD000007; Clg_helix; 2.
DR Hypothetical protein.
KW SEQUENCE 678 AA; 67182 MW; 9771D3E0CA95B3D7 CRC64;

Query Match          52.0%; Score 205; DB 9; Length 678;
Best Local Similarity 54.3%; Pred.No.1.7e-13;
Matches 38; Conservative 11; Mismatches 21; Indels 0; Gaps 0;

QY      1  GPKGDGDEKDPDPEEGKHGVGRMPKGIGKELGDMGDGRGNIGKTGPIGKKDKGEKGLL 60
DB      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
247  GPQGSETPGKDVGVPKGKETPVGPQQGAPGPKGERGVGAAGVAPGPRGKEGQERGFQ 306

QY      61  GPIGEKGKAG 70
DB      |||::|||

307  GIPLKGDGTG 316

RESULT 11

```

Q9GQB1 PRELIMINARY; PRT; 1723 AA.

AC Q9GQB1  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Type IV collagen alpha 1 chain precursor.  
OS Hydra attenuata (Hydra) (Hydra vulgaris).  
OC Eukaryota; Metazoa; Chordata; Hydrozoa; Hydrozoa; Anthomedusae;  
OC Hydridae; Hydra.  
OX NCBI\_TaxID=6087;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20564332; PubMed=10956657;  
RA Fowler S.J., Jose S., Zhang X., Deutzmann R., Sarraz M.P. Jr.,  
RA Boot-Handford R.P.;  
RT "Characterization of hydra type IV collagen: Type IV collagen is  
RT essential for head regeneration and its expression is up-regulated  
RT upon exposure to glucose."  
RL J. Biol. Chem. 275:39589-39599(2000).  
DR EMBL: AF282902; AAG40729.1; -;  
DR GO: 0005581; C:collagen; IEA.  
DR GO: 0005201; F:extracellular matrix structural constituent; IEA.  
DR InterPro: IPR008161; Clg\_helix.  
DR InterPro: IPR008160; Collagen.  
DR InterPro: IPR001442; Procollagen4\_C.  
DR Pfam: PF01413; C4; 2.  
DR ProDom: PD000007; Clg\_helix; 6.  
DR ProDom: PD003923; Procollagen4; 1.  
DR SMART: SM00111; C4; 2.  
DR Collagen; Signal.  
KW SIGNAL.  
FT SIGNAL.  
SQ SEQUENCE 1723 AA; 168996 MW; 92496D62FD162F01 CRC64;

Query Match 49.7%; Score 196; DB 5; Length 1723;  
Best Local Similarity 38.9%; Pred. No. 4.2e-12;  
Matches 42; Conservative 13; Mismatches 15; Indels 38; Gaps 3;

QY 1 GPKGDDGKGGDP---GEKGKGVGRMGPKGKGE-----LQDMGDRGNIGKTG 46  
Db 173 GPKSQDGPAGDPGTGDKGSGKAGRMGPGQLRGKRGAGDSNITIFGERGDKDGLPG 232  
QY 47 P-----IGKKDKGKGLLIGIPGKGGKAG 70  
Db 233 PPRDCNGSSVTGELITNIQPKGQKGGQKGGQKGGQKGGQKGGQKGGQKGGQKGG 280

RESULT 12

Q9AGC4 PRELIMINARY; PRT; 465 AA.

AC Q9AGC4  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Collagen-like protein B (Fragment).  
OS Streptococcus pyogenes.  
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;  
OC Streptococcus.  
OX NCBI\_TaxID=1314;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX STRAIN=AP55;  
RA Rasmussen M., Bjorck L.;  
RT "Phase-variation of a novel collagen-like surface protein in  
RT Streptococcus pyogenes."  
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF336819; AAK30079.1; -;  
DR InterPro: IPR008161; Clg\_helix.  
DR InterPro: IPR008160; Collagen.  
DR Pfam: PF01391; Collagen; 5.  
DR ProDom: PD000007; Clg\_helix; 1.  
NON\_TER 465 465

QY 1 GPKGDDGKGGDPGEGKGVGRMGPKGKGE-----GKGLGDMGDRGNIGKTGPI 48  
Db 113 GSKGDPGKGGDPGEGKGVGRMGPKGKGE-----GKGLGDMGDRGNIGKTGPI 172

QY 49 GKKGDKGKGLL-----GIPGKGGKAG 70  
Db 173 GSKGDPGKGGKATGQVGRGKGGKGGKGGKGGKGGKGGKGGKGGKGGKGGKGGKGG 203

RESULT 13

Q8QTH5 PRELIMINARY; PRT; 465 AA.

AC Q8QTH5  
DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE WSSV021.  
OS White spot syndrome virus (WSSV).  
OC Viruses; dsDNA viruses, no RNA stage; Nimaviridae.  
OX NCBI\_TaxID=92652;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX STRAIN=Taiwan;  
RX MEDLINE=20517548; PubMed=11062040;  
RA Tsai M.F., Yu H.T., Tzeng H.F., Leu J.H., Chou C.M., Huang C.J.,  
RA Wang C.H., Lin J.Y., Kou G.H., Lo C.F.;  
RT "Identification and characterization of a shrimp white spot syndrome  
RT virus (WSSV) gene that encodes a novel chimeric polypeptide of  
RT cellular-type thymidine kinase and thymidylate kinase."  
RL Virology 277:100-110(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX STRAIN=Taiwan;  
RX MEDLINE=21844071; PubMed=11853398;  
RA Chen L.L., Leu J.H., Huang C.J., Chou C.M., Chen S.M., Wang C.H.,  
RA Lo C.F., Kou G.H.;  
RT "Identification of a nucleocapsid protein (VP35) gene of shrimp white  
RT spot syndrome virus and characterization of the motif important for  
RT targeting VP35 to the nuclei of transfected insect cells."  
RL Virology 293:44-53(2002).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX STRAIN=Taiwan;  
RA Lo C.F., Kou G.-H.;  
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF440570; AAL88889.1; -;  
DR InterPro: IPR008160; Collagen.  
DR Pfam: PF01391; Collagen; 2.  
SQ SEQUENCE 465 AA; 53009 MW; 435F1A3488B83BD5 CRC64;

Query Match 49.5%; Score 195; DB 12; Length 465;  
Best Local Similarity 52.9%; Pred. No. 1.3e-12;  
Matches 37; Conservative 12; Mismatches 21; Indels 0; Gaps 0;

QY 1 GPKGDDGKGGDPGEGKGVGRMGPKGKGE-----GKGLGDMGDRGNIGKTGPIGKGGKGGKGLL 60  
Db 19 GSKGDKGKGG 78

QY 61 GIPGKGGKAG 70  
Db 79 GSKGDKGKGG 88

RESULT 14

Q9BWP8 PRELIMINARY; PRT; 271 AA.

ID Q9BWP8  
AC Q9BWP8

DT 01-JUN-2001 (TRENBLrel. 17, Created)  
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)  
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RA Strausberg R.;  
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC000078; AAH00078.1; -.  
DR HSSP; P22897; IEGS.  
DR GO; GO:0005529; F:sugar binding; IEA.  
DR InterPro; IPR008160; Collagen.  
DR InterPro; IPR001304; Lectin C.  
DR Pfam; PF01391; Collagen; 1.  
DR Pfam; PF00059; lectin c; 1.  
DR SMART; SM00034; CLECT; 1.  
DR PROSITE; PS00615; C\_TYPE\_LECTIN\_1; 1.  
DR PROSITE; PS00041; C\_TYPE\_LECTIN\_2; 1.  
KW Hypothetical protein.  
SQ SEQUENCE 271 AA; 28665 MW; A14A248CE41DB340 CRC64;

Query Match 49.2%; Score 194; DB 4; Length 271;  
Best Local Similarity 52.1%; Pred. No. 8.8e-13;  
Matches 38; Conservative 12; Mismatches 17; Indels 6; Gaps 2;  
QY 1 GPKGDGEGKDGKGVGMGPKIKGELGDMGDRGNI---GKTGPIGKKGKGEK 57  
DB 41 GLKGDAGEKGD---KGAPGRGVGTGKGMGDKQKQSVGRHKGPIGSKGEKGS 97

QY 58 GLGIPGEGKAG 70  
DB 93 GDIGPFENGEPG 110

RESULT 15  
Q9P690 PRELIMINARY; PRT; 291 AA.  
AC Q9P690;  
DT 01-MAR-2001 (TRENBLrel. 16, Created)  
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)  
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)  
DE Collagen-like surface protein (Fragment).  
OS Streptococcus pyogenes.  
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;  
OC Streptococcus.  
OX NCBI\_TaxID=1314;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=AP15;  
RX MEDLINE=20490571; PubMed=11035747;  
RA Rasmussen M., Eden A., Bjorck L.;  
RT "SclA, a novel collagen-like surface protein of streptococcus pyogenes.";  
RL Infect. Immun. 68:6370-6377(2000).  
DR EMBL; AF296333; AAG30213.1; -.  
DR InterPro; IPR008160; Collagen.  
DR Pfam; PF01391; Collagen; 1.  
DR NON\_TER 1  
FT NON\_TER 291 291  
SQ SEQUENCE 291 AA; 31100 MW; E879218AEA003349 CRC64;

Query Match 49.1%; Score 193.5; DB 2; Length 291;  
Best Local Similarity 53.4%; Pred. No. 1.1e-12;  
Matches 39; Conservative 7; Mismatches 24; Indels 3; Gaps 1;  
QY 1 GPKGDGEGKGD---PGEKGKGVGMGPKIKGELGDMGDRGNI---GKTGPIGKKGKGEK 57  
DB 130 GPKGDRGEGKDTGATGPGGAGKDGAPGKGDGKDRGEGTGAQGPVGPQGEKGET 189

QY 58 GLGIPGEGKAG 70  
DB 190 GAQGPAGPQGEAG 202  
Search completed: March 8, 2004, 12:15:12  
Job time : 57.1894 secs

Result No.	Query %	Score	Match	Length	DB	ID	Description
1	196	49.7	689	1	CA29	HUMAN	Q14055 homo sapien
2	193	49.0	688	1	CA29	MOUSE	Q07643 mus musculu
3	186.5	47.3	1775	1	CA14	DROME	P08120 drosophila
4	184.5	46.8	1366	1	CA21	HUMAN	P08123 homo sapien
5	182	46.2	1736	1	CA22	MOUSE	Q64739 mus musculu
6	181	45.9	518	1	MT00	MOUSE	Q60754 mus musculu
7	180.5	45.8	508	1	OT01	ONCKE	P83371 oncorhynch
8	179.5	45.6	2944	1	CA17	HUMAN	Q02388 homo sapien
9	179	45.4	1028	1	CA16	HUMAN	P12109 homo sapien
10	178.5	45.3	289	1	CO17	HUMAN	Q9bxj2 homo sapien
11	178.5	45.3	674	1	CA1A	CHICK	P08125 gallus gall
12	177.5	45.1	1362	1	CA21	CHICK	P02467 gallus gall
13	176.5	44.8	1019	1	CA16	CHICK	P20785 gallus gall
14	176.5	44.8	1364	1	CA21	BOVIN	P02465 bos taurus
15	176.5	44.8	1804	1	CA1B	HUMAN	Q61245 mus musculu
16	176	44.7	547	1	CAFL	SPHNU	P18856 ephydratia m
17	175	44.4	371	1	CL46	BOVIN	Q8mhz9 bos taurus
18	175	44.3	374	1	PSPD	RAT	P35248 rattus norv
19	174.5	44.3	375	1	PSPD	HUMAN	P35247 homo sapien
20	174.5	44.3	1025	1	CA16	MOUSE	OC4857 mus musculu
21	174	44.2	1355	1	CA21	RANCA	Q42350 rana catesb
22	174	44.2	1659	1	CA14	HUMAN	P02462 homo sapien
23	174	44.2	1838	1	CA15	HUMAN	P20908 homo sapien
24	173.5	44.0	1366	1	CA21	CANFA	Q46392 canis fami
25	173.5	44.0	1496	1	CA25	HUMAN	P05997 homo sapien
26	172.5	43.8	1037	1	CAFP	RIFPA	P30754 riftia pach
27	172.5	43.8	1745	1	CA35	HUMAN	P25940 homo sapien
28	172	43.7	1262	1	CA13	CHICK	P12105 gallus gall
29	171.5	43.5	1372	1	CA21	MOUSE	Q01149 mus musculu
30	171.	43.4	520	1	MRCO	HUMAN	Q9uew3 homo sapien
31	171	43.4	1736	1	CA2B	HUMAN	P13942 homo sapien
32	170.5	43.3	483	1	MRCO	MEASU	Q9wub9 mesocricetu
33	170.5	43.3	1418	1	CA12	HUMAN	P02458 homo sapien



Matches 37; Conservative 14; Mismatches 19; Indels 12; Gaps 1;  
QY 1 GKXGDDGKGDGE-----BKHKGVKMGPKGKGLGDMGRGNIGTKGPI 48  
DB 342 GTKGFGDKGEGQGLPGVGFPGKEGPGPRGEIGQGMQKGQGRGVGPGGPQ 401  
QY 49 GKXGDKGKGLGIPGEGKAG 70  
DB 402 GRQGPKGEGPGIPGPGQLPG 423  
RESULT 3  
CA14 DROME STANDARD; PRT; 1775 AA.  
AC P08120;  
DT 01-AUG-1988 (Rel. 08, Created)  
DT 01-NOV-1990 (Rel. 16, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Collagen alpha 1(IV) chain precursor.  
GN CG25C OR DCG1.  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=89054012; PubMed=3142875;  
RA Blumberg B., Mackrell A.J., Fessler J.H.;  
RT "Drosophila basement membrane procollagen alpha 1(IV). II. Complete  
RT cDNA sequence, genomic structure, and general implications for  
RT supramolecular assemblies.";  
RL J. Biol. Chem. 263:18328-18337(1988).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX Blumberg B.;  
RA Thesis (1987), University of California / Los Angeles, U.S.A.  
RN [3]  
RP SEQUENCE FROM N.A.  
RA Mackrell A.J.;  
RN Thesis (1992), University of California / Los Angeles, U.S.A.  
RP SEQUENCE OF 1065-1775 FROM N.A.  
RX MEDLINE=87194801; PubMed=3106346;  
RA Blumberg B., Mackrell A.J., Olson P.F., Kurkinen M., Monson J.M.,  
RA Natzie J.E., Fessler J.H.;  
RT "Basement membrane procollagen IV and its specialized carboxyl domain  
RT are conserved in Drosophila, mouse, and human.";  
RL J. Biol. Chem. 262:5947-5950(1987).  
RN [5]  
RP SEQUENCE OF 1355-1775 FROM N.A.  
RX MEDLINE=87246644; PubMed=3109906;  
RA Cecchini J.P., Knibiehler B., Mirre C., le Parco Y.;  
RT "Evidence for a type-IV-related collagen in Drosophila melanogaster.  
RT Evolutionary constancy of the carboxyl-terminal noncollagenous  
RT domain.";  
RL Eur. J. Biochem. 165:587-593(1987).  
RN [6]  
RP SEQUENCE OF 762-1230 FROM N.A.  
RX MEDLINE=82197577; PubMed=6210912;  
RA Monson J.M., Natzie J., Friedman J., McCarthy B.J.;  
RT "Expression and novel structure of a collagen gene in Drosophila.";  
RL Proc. Natl. Acad. Sci. U.S.A. 79:1761-1765(1982).  
CC -1- FUNCTION: Collagen type IV is specific for basement membranes.  
CC -1- SUBUNIT: Trimers of two alpha 1(IV) and one alpha 2(IV) chain.  
CC Type IV collagen forms a mesh-like network linked through  
CC intermolecular interactions between 7S domains and between NCI  
CC domains.  
CC -1- DOMAIN: Alpha chains of type IV collagen have a noncollagenous  
CC domain (NC1) at their C-terminus, frequent interruptions of the G-  
CC X-Y repeats in the long central triple-helical domain (which may  
CC cause flexibility in the triple helix), and a short N-terminal  
CC triple-helical 7S domain.

-1- PTM: Prolines at the third position of the tripeptide repeating  
CC unit (G-X-Y) are hydroxylated in some or all of the chains.  
CC -1- PTM: Type IV collagens contain numerous cysteine residues which  
CC are involved in inter- and intramolecular disulfide bonding. 12 of  
CC these, located in the NC1 domain, are conserved in all known type  
CC IV collagens.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
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CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
CC -----  
CC EMBL; M23704; AAA28404.1; -;  
DR EMBL; M96575; AAB59184.1; -;  
DR EMBL; J02727; AAA28423.1; -;  
DR EMBL; M28334; AAA28422.1; -;  
DR EMBL; V00200; CAA23486.2; -;  
DR PIR; A31893; A31893.  
DR FlyBase; FBgn0000289; Cg25C.  
DR GO; GO:0005597; C:collagen type IV; NAS.  
DR InterPro; IPR008161; Clg\_helix.  
DR InterPro; IPR008160; Collagen.  
DR Pfam; PF01413; C4; 2.  
DR Pfam; PF01391; Collagen; 25.  
DR ProDom; PD000007; Clg\_helix; 9.  
DR ProDom; PD003923; ProcollagnC4; 1.  
DR SMART; SM00111; C4; 2.  
KW Extracellular matrix; Connective tissue; Basement membrane;  
KW Repeat; Hydroxylation; Glycoprotein; Collagen; Signal.  
FT SIGNAL 1 23  
FT PROPEP 24 ?  
FT CHAIN ? 1775 AMINO-TERMINAL PROPEPTIDE (7S DOMAIN).  
FT DOMAIN ? 1544 COLLAGEN ALPHA 1(IV) CHAIN.  
FT DOMAIN 1545 1775 TRIPLE-HELICAL REGION.  
FT DISULFID 1549 1655 NONHELICAL REGION (NC1).  
FT DISULFID 1569 1655 OR 1652 (BY SIMILARITY).  
FT DISULFID 1599 1652 OR 1655 (BY SIMILARITY).  
FT DISULFID 1611 1617 BY SIMILARITY.  
FT DISULFID 1674 1770 OR 1767 (BY SIMILARITY).  
FT DISULFID 1708 1767 OR 1770 (BY SIMILARITY).  
FT DISULFID 1720 1727 BY SIMILARITY.  
FT CARBOHYD 72 72 N-LINKED (GLCNAC... ) (PROBABLE).  
FT CONFLICT 948 948 L -> S (IN REF. 6).  
FT CONFLICT 997 997 S -> T (IN REF. 6).  
FT CONFLICT 1357 1357 Q -> K (IN REF. 5).  
FT CONFLICT 1360 1360 Q -> K (IN REF. 5).  
FT CONFLICT 1373 1373 T -> I (IN REF. 5).  
FT CONFLICT 1496 1496 L -> R (IN REF. 5).  
FT CONFLICT 1507 1511 ETGNV -> RAGOR (IN REF. 5).  
FT CONFLICT 1529 1529 E -> K (IN REF. 5).  
FT CONFLICT 1733 1733 M -> I (IN REF. 5).  
SQ SEQUENCE 1775 AA; 174119 MW; 2D5EAB23149525CD CRC64;  
Query Match 47.3%; Score 186.5; DB 1; Length 1775;  
Best Local Similarity 46.8%; Pred. No. 5.7e-11;  
Matches 37; Conservative 10; Mismatches 23; Indels 9; Gaps 1;  
QY 1 GKXGDDGE-----KGDGEGKGVKGMGPKGKGLGDMGRGNIGTKGPI 51  
DB 295 GPRGDMGQGRGFGVLVGRGEGPGEGTGLDQKGEKGLPGGPRGGRGQGNFGPGGTGQK 354  
QY 52 GDKGEGKGLGIPGEGKAG 70  
DB 355 GDRGEGFLGFLGPNPGQKG 373  
RESULT 4  
CA21 HUMAN STANDARD; PRT; 1366 AA.  
ID CA21 HUMAN  
AC P08123; P02464; Q9UEB6; Q9UPH0;



DT 01-AUG-1988 (Rel. 08, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Collagen alpha 2(I) chain precursor.  
GN COL1A2.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RN SEQUENCE FROM N.A.  
RX MEDLINE=8058962; PubMed=2824475;  
RA de Wet W.J., Bernard M.P., Benson-Chanda V., Chu M.-L., Dickson L.A.,  
RA Weil D., Ramirez F.;  
RA "Organization of the human pro-alpha 2(I) collagen gene.";  
RL J. Biol. Chem. 262:16032-16036(1987).  
RN [2]  
RN SEQUENCE FROM N.A.  
RA Korkko J.M., Earley J.J., Ala-Kokko L., Prockop D.J.;  
RA "Analysis of the COL1A1 and COL1A2 genes by CSGE and DNA sequencing in  
RT 14 patients with mild OI (Type I). Identification of common sequences  
RT for null allele mutations.";  
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RN SEQUENCE OF 1-765 FROM N.A.  
RC TISSUE=Placenta;  
RX MEDLINE=88339824; PubMed=3421913;  
RA Kuivaniemi H., Tromp G., Chu M.-L., Prockop D.J.;  
RA "Structure of a full-length cDNA clone for the propro alpha 2(I)  
RT chain of human type I procollagen. Comparison with the chicken gene  
RT confirms unusual patterns of gene conservation.";  
RL Biochem. J. 252:633-640(1988).  
RN [4]  
RN SEQUENCE OF 181-1366 FROM N.A.  
RA Kalicki J., Wamsley P., Gibson A.;  
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RN SEQUENCE OF 623-1366 FROM N.A.  
RX MEDLINE=83178919; PubMed=6687691;  
RA Bernard M.P., Myers J.C., Chu M.-L., Ramirez F., Eikenberry E.F.,  
RA Prockop D.J.;  
RA "Structure of a cDNA for the pro alpha 2 chain of human type I  
RT procollagen. Comparison with chick cDNA for pro alpha 2(I) identifies  
RT structurally conserved features of the protein and the gene.";  
RL Biochemistry 22:1139-1145(1983).  
RN [6]  
RN SEQUENCE OF 80-96.  
RC TISSUE=Skin;  
RX MEDLINE=71038625; PubMed=5529814;  
RA Click E.M., Bornstein P.;  
RA "Isolation and characterization of the cyanogen bromide peptides from  
RT the alpha 1 and alpha 2 chains of human skin collagen.";  
RL Biochemistry 9:4693-4706(1970).  
RN [7]  
RN SEQUENCE OF 417-447.  
RC TISSUE=Skin;  
RX MEDLINE=75008198; PubMed=4412529;  
RA Fietzek P.P., Furthmayr H., Kuehn K.;  
RA "Comparative sequence studies on alpha2-CB2 from calf, human, rabbit  
RT and pig-skin collagen.";  
RL Eur. J. Biochem. 47:257-261(1974).  
RN [8]  
RN SEQUENCE OF 145-198 FROM N.A.  
RX MEDLINE=88298792; PubMed=3403536;  
RA Kuivaniemi H., Sabo C., Tromp G., Sippola-Thiele M., Prockop D.J.;  
RA "A 19-base pair deletion in the pro-alpha 2(I) gene of type I  
RT procollagen that causes in-frame RNA splicing from exon 10 to exon 12  
RT in a proband with atypical osteogenesis imperfecta and in his  
RT asymptomatic mother.";  
RL J. Biol. Chem. 263:11407-11413(1988).  
RN [9]  
RN SEQUENCE OF 960-1351 FROM N.A.  
RC TISSUE=Skin;  
RX MEDLINE=90304220; PubMed=2364107;  
RA Maekelae J.K., Vuorio T., Vuorio E.;  
RA "Growth-dependent modulation of type I collagen production and mRNA  
RT levels in cultured human skin fibroblasts.";  
RL Biochim. Biophys. Acta 1049:171-176(1990).  
RN [10]  
RN REVIEW ON VARIANTS.  
RX MEDLINE=91184577; PubMed=2010058;  
RA Kuivaniemi H., Tromp G., Prockop D.J.;  
RA "Mutations in collagen genes: causes of rare and some common diseases  
RT in humans.";  
RL PASEB J. 5:2052-2060(1991).  
RN [11]  
RN REVIEW ON VARIANTS.  
RX MEDLINE=97255959; PubMed=3101290;  
RA Kuivaniemi H., Tromp G., Prockop D.J.;  
RA "Mutations in fibrillar collagens (types I, II, III, and XI), fibril-  
RT associated collagen (type IX), and network-forming collagen (type X)  
RT cause a spectrum of diseases of bone, cartilage, and blood vessels.";  
RL Hum. Mutat. 9:300-315(1997).  
RN [12]  
RN REVIEW ON OI VARIANTS.  
RX MEDLINE=91374476; PubMed=1895312;  
RA Byers P.H., Wallis G.A., Willing M.C.;  
RA "Osteogenesis imperfecta: translation of mutation to phenotype.";  
RL J. Med. Genet. 28:433-442(1991).  
RN [13]  
RN REVIEW ON OI VARIANTS.  
RX MEDLINE=97169389; PubMed=9016532;  
RA Dalgleish R.;  
RA "The human type I collagen mutation database.";  
RL Nucleic Acids Res. 25:181-187(1997).  
RN [14]  
RN VARIANT EDS-VII-A2.  
RX MEDLINE=88059013; PubMed=3680255;  
RA Wirtz M.K., Glanville R.W., Steinmann B., Rao V.H., Hollister D.W.;  
RA "Ehlers-Danlos syndrome type VIIb. Deletion of 18 amino acids  
RT comprising the N-telopeptide region of a pro-alpha 2(I) chain.";  
RL J. Biol. Chem. 262:16376-16385(1987).  
RN [15]  
RN SEQUENCE OF 1090-1107 FROM N.A., AND VARIANT OI-IV ARG-1102.  
RX MEDLINE=88227975; PubMed=2897363;  
RA Wenstrup R.J., Cohn D.H., Cohen T., Byers P.H.;  
RA "Arginine for glycine substitution in the triple-helical domain of  
RT the products of one alpha 2(I) collagen allele (COL1A2) produces the  
RT osteogenesis imperfecta type IV phenotype.";  
RL J. Biol. Chem. 263:7734-7740(1988).  
RN [16]  
RN VARIANT OI-II ASP-997.  
RX MEDLINE=89123407; PubMed=2914942;  
RA Baldwin C.T., Constantinou C., Dumars K.W., Prockop D.J.;  
RA "A single base mutation that converts glycine 907 of the alpha 2(I)  
RT chain of type I procollagen to aspartate in a lethal variant of  
RT osteogenesis imperfecta. The single amino acid substitution near the  
RT carboxyl terminus destabilizes the whole triple helix.";  
RL J. Biol. Chem. 264:3002-3006(1989).  
RN [17]  
RN VARIANT OI-II SER-955.  
RX MEDLINE=89380165; PubMed=2777764;  
RA Lamande S.R., Dahl H.-H.M., Cole W.G., Bateman J.F.;  
RA "Characterization of point mutations in the collagen COL1A1 and  
RT COL1A2 genes causing lethal perinatal osteogenesis imperfecta.";  
RL J. Biol. Chem. 264:15809-15812(1989).  
RN [18]  
RN VARIANT OI-II CYS-877.  
RA Firtala A., Westerhausen A., Morris G.M., Rooney J.E., Prockop D.J.;  
RA "Two cysteine substitutions in the type I procollagen genes (COL1A1  
RT and COL1A2) that cause lethal osteogenesis imperfecta. The location  
RT of glycine substitutions does not in any simple way predict their  
RT effects on protein function or phenotype.";  
RL Am. J. Hum. Genet. 47:A216-A216(1990).  
RN [19]  
RN VARIANT EDS-VII-A2.  
RX MEDLINE=90304220; PubMed=2364107;  
RA Maekelae J.K., Vuorio T., Vuorio E.;  
RA "Growth-dependent modulation of type I collagen production and mRNA  
RT levels in cultured human skin fibroblasts.";  
RL Biochim. Biophys. Acta 1049:171-176(1990).  
RN [10]  
RN REVIEW ON VARIANTS.  
RX MEDLINE=91184577; PubMed=2010058;  
RA Kuivaniemi H., Tromp G., Prockop D.J.;  
RA "Mutations in collagen genes: causes of rare and some common diseases  
RT in humans.";  
RL PASEB J. 5:2052-2060(1991).  
RN [11]  
RN REVIEW ON VARIANTS.  
RX MEDLINE=97255959; PubMed=3101290;  
RA Kuivaniemi H., Tromp G., Prockop D.J.;  
RA "Mutations in fibrillar collagens (types I, II, III, and XI), fibril-  
RT associated collagen (type IX), and network-forming collagen (type X)  
RT cause a spectrum of diseases of bone, cartilage, and blood vessels.";  
RL Hum. Mutat. 9:300-315(1997).  
RN [12]  
RN REVIEW ON OI VARIANTS.  
RX MEDLINE=91374476; PubMed=1895312;  
RA Byers P.H., Wallis G.A., Willing M.C.;  
RA "Osteogenesis imperfecta: translation of mutation to phenotype.";  
RL J. Med. Genet. 28:433-442(1991).  
RN [13]  
RN REVIEW ON OI VARIANTS.  
RX MEDLINE=97169389; PubMed=9016532;  
RA Dalgleish R.;  
RA "The human type I collagen mutation database.";  
RL Nucleic Acids Res. 25:181-187(1997).  
RN [14]  
RN VARIANT EDS-VII-A2.  
RX MEDLINE=88059013; PubMed=3680255;  
RA Wirtz M.K., Glanville R.W., Steinmann B., Rao V.H., Hollister D.W.;  
RA "Ehlers-Danlos syndrome type VIIb. Deletion of 18 amino acids  
RT comprising the N-telopeptide region of a pro-alpha 2(I) chain.";  
RL J. Biol. Chem. 262:16376-16385(1987).  
RN [15]  
RN SEQUENCE OF 1090-1107 FROM N.A., AND VARIANT OI-IV ARG-1102.  
RX MEDLINE=88227975; PubMed=2897363;  
RA Wenstrup R.J., Cohn D.H., Cohen T., Byers P.H.;  
RA "Arginine for glycine substitution in the triple-helical domain of  
RT the products of one alpha 2(I) collagen allele (COL1A2) produces the  
RT osteogenesis imperfecta type IV phenotype.";  
RL J. Biol. Chem. 263:7734-7740(1988).  
RN [16]  
RN VARIANT OI-II ASP-997.  
RX MEDLINE=89123407; PubMed=2914942;  
RA Baldwin C.T., Constantinou C., Dumars K.W., Prockop D.J.;  
RA "A single base mutation that converts glycine 907 of the alpha 2(I)  
RT chain of type I procollagen to aspartate in a lethal variant of  
RT osteogenesis imperfecta. The single amino acid substitution near the  
RT carboxyl terminus destabilizes the whole triple helix.";  
RL J. Biol. Chem. 264:3002-3006(1989).  
RN [17]  
RN VARIANT OI-II SER-955.  
RX MEDLINE=89380165; PubMed=2777764;  
RA Lamande S.R., Dahl H.-H.M., Cole W.G., Bateman J.F.;  
RA "Characterization of point mutations in the collagen COL1A1 and  
RT COL1A2 genes causing lethal perinatal osteogenesis imperfecta.";  
RL J. Biol. Chem. 264:15809-15812(1989).  
RN [18]  
RN VARIANT OI-II CYS-877.  
RA Firtala A., Westerhausen A., Morris G.M., Rooney J.E., Prockop D.J.;  
RA "Two cysteine substitutions in the type I procollagen genes (COL1A1  
RT and COL1A2) that cause lethal osteogenesis imperfecta. The location  
RT of glycine substitutions does not in any simple way predict their  
RT effects on protein function or phenotype.";  
RL Am. J. Hum. Genet. 47:A216-A216(1990).  
RN [19]  
RN VARIANT EDS-VII-A2.

EX MEDLINE=90368825; PubMed=2394758;  
RA Weil D., D'Alessio M., Ramirez F., Eyre D.R.;  
RT "Structural and functional characterization of a splicing mutation in  
RT the pro-alpha 2(I) collagen gene of an Ehlers-Danlos type VII  
RT patient.";  
RL J. Biol. Chem. 265:16007-16011(1990).  
RN [20]  
RP VARIANT OI-IV VAL-676.  
RX MEDLINE=91291136; PubMed=2064612;  
RA Bateman J.F., Hannagan M., Chan D., Cole W.G.;  
RT "Characterization of a type I collagen alpha 2(I) glycine-586 to  
RT valine substitution in osteogenesis imperfecta type IV. Detection of  
RT the mutation and prenatal diagnosis by a chemical cleavage method.";  
RL Biochem. J. 276:765-770(1991).  
RN [21]  
RP VARIANTS OI CYS-349 AND CYS-736.  
RX MEDLINE=91115889; PubMed=1990009;  
RA Wensurup R.J., Shrago-Howe A.W., Lever L.W., Phillips C.L.,  
RA Byers P.H., Cohn D.H.;  
RT "The effects of different cysteine for glycine substitutions within  
RT alpha 2(I) chains. Evidence of distinct structural domains within the  
RT type I collagen triple helix.";  
RL J. Biol. Chem. 266:2590-2594(1991).  
RN [22]  
RP VARIANT OI-II ARG-784.  
RX MEDLINE=91340689; PubMed=1874719;  
RA Tsuneyoshi T., Westerhausen A., Constantinou C.D., Prockop D.J.;  
RT "Substitutions for glycine alpha 1-637 and glycine alpha 2-694 of  
RT type I procollagen in lethal osteogenesis imperfecta. The  
RT conformational strain on the triple helix introduced by a glycine  
RT substitution can be transmitted along the helix.";  
RL J. Biol. Chem. 266:15608-15613(1991).  
RN [23]  
RP VARIANT OI-IV SER-751.  
RX MEDLINE=91271401; PubMed=2052622;  
RA Spotila L.D., Constantinou C.D., Sereda L., Ganguly A., Riggs B.L.,  
RA Prockop D.J.;  
RT "Mutation in a gene for type I procollagen (COL1A2) in a woman with  
RT postmenopausal osteoporosis: evidence for phenotypic and genotypic  
RT overlap with mild osteogenesis imperfecta.";  
RL Proc. Natl. Acad. Sci. U.S.A. 88:5423-5427(1991).  
RN [24]  
RP VARIANT OI-II ARG-547.  
RX MEDLINE=93244832; PubMed=1284475;  
RA Bateman J.F., Moeller I., Hannagan M., Chan D., Cole W.G.;  
RT "Lethal perinatal osteogenesis imperfecta due to a type I collagen  
RT alpha 2(I) Gly to Arg substitution detected by chemical cleavage of  
RT an mRNA: cDNA sequence mismatch.";  
RL Hum. Mutat. 1:55-62(1992).  
RN [25]  
RP VARIANT OI-II ASP-670.  
RX MEDLINE=93054637; PubMed=1385413;  
Query Match 46.8%; Score 184.5; DB 1; Length 1366;  
Best Local Similarity 42.9%; Pred. No. 7e-11;  
Matches 39; Conservative 9; Mismatches 22; Indels 21; Gaps 2;  
Qy 1 GPXGDGEGKDDPGEKGVKMPKGIKBLGDMGRNIGTGPICKK----- 51  
Db 559 GPSGPGAGEVKGPGERGLHGFGLPGAPGRGPPGSGAAGTGPIGSRGSGPPGPD 618  
Qy 52 GDKGEKGLL-----GIPGEKKGAG 70  
Db 619 GNKGEGVGVGAVTACPSGSLPGERGAG 649  
RESULT 5  
CA2B MOUSE  
ID CA2B.MOUSE STANDARD; PRT; 1736 AA.  
AC Q64739; Q61432; Q921W0;  
DT 15-JUL-1998 (Rel. 36, Created)  
DI 10-OCT-2003 (Rel. 42, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Collagen alpha 2(XI) chain precursor.  
GN COL1A2.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
ON NCBI\_TaxID=10090;  
RX [1]  
RP SEQUENCE FROM N.A. (ISOFORM 7).  
RC STRAIN=129/SV;  
RA Rowen L., Qin S., Madan A., Loretz C., James R., Dors M., Vix L.,  
RA Hall J., Lasky S., Hood L.;  
RT "Sequence of the mouse major histocompatibility locus class II  
RT region.";  
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE OF 1-1678 FROM N.A. (ISOFORM 7).  
RC STRAIN=FVB/N, and 129/SV; TISSUE=Cartilage;  
RX MEDLINE=91135795; PubMed=8981332;  
RA Vandenberg P., Vuoristo M.M., Ala-Kokko L., Prockop D.J.;  
RT "The mouse coll1a2 gene. Some transcripts from the adjacent rxr-beta  
RT gene extend into the coll1a2 gene.";  
RL Matrix Biol. 15:359-367(1996).  
RN [3]  
RP SEQUENCE OF 1-624 FROM N.A. (ISOFORMS 1; 2; 3; 4; 5 AND 6).  
RC STRAIN=129/SV;  
RX MEDLINE=95138212; PubMed=7836472;  
RA Tsunaki N., Kimura T.;  
RT "Differential expression of an acidic domain in the amino-terminal  
RT propeptide of mouse pro-alpha2(XI) collagen by complex alternative  
RT splicing.";  
RL J. Biol. Chem. 270:2372-2378(1995).  
RN [4]  
RP SEQUENCE OF 1-8 FROM N.A.  
RC STRAIN=129/SV; TISSUE=Liver;  
RX MEDLINE=96427460; PubMed=8830784;  
RA Tsunaki N., Kimura T., Mateui Y., Ochi T.;  
RT "Separable cis-regulatory elements that contribute to tissue- and  
RT site-specific alpha 2(XI) collagen gene expression in the embryonic  
RT mouse cartilage.";  
RL J. Cell Biol. 134:1573-1582(1996).  
RN [5]  
RP FUNCTION: May play an important role in fibrillogenesis by  
RP controlling lateral growth of collagen II fibrils (By similarity).  
CC -!- SUBUNIT: Trimers composed of three different chains: alpha 1(XI),  
CC alpha 2(XI), and alpha 3(XI). Alpha 3(XI) is a post-translational  
CC modification of alpha 1(XI). Alpha 1(XI) can also be found instead  
CC of alpha 3(XI)=1(III) (By similarity).  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event-Alternative splicing; Named isoforms=7;  
CC Comment-Additional isoforms seem to exist;  
CC Name=1; Synonyms=E56789;  
CC IsoId=Q64739-2; Sequence=Displayed;  
CC Name=2; Synonyms=E5689;  
CC IsoId=Q64739-3; Sequence=VSP\_007346;  
CC Name=3; Synonyms=E5789;  
CC IsoId=Q64739-4; Sequence=VSP\_007345;  
CC Name=4; Synonyms=E569;  
CC IsoId=Q64739-5; Sequence=VSP\_007346; VSP\_007347;  
CC Name=5; Synonyms=E589;  
CC IsoId=Q64739-6; Sequence=VSP\_007345; VSP\_007346;  
CC Name=6; Synonyms=E59;  
CC IsoId=Q64739-7; Sequence=VSP\_007345; VSP\_007346; VSP\_007347;  
CC Name=7;  
CC IsoId=Q64739-1; Sequence=VSP\_007345; VSP\_007347;  
CC -!- PTM: Prolines at the third position of the tripeptide repeating  
CC unit (G-X-Y) are hydroxylated in some or all of the chains.  
CC -!- SIMILARITY: BELONGS TO THE FIBRILLAR CLASS OF COLLAGENS.  
CC -!- SIMILARITY: Contains 1 TSP N-terminal (TSPN) domain.  
CC -----  
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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CC use by non-profit institutions as long as its content is in no way  
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AC Q60754;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Macrophage receptor MARCO (Macrophage receptor with collagenous structure).  
GN MARCO.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=95171455; PubMed=7867067;  
RA Elomaa O., Kangas M., Sahiberg C., Tuukkanen J., Sormunen R., Liakka A., Thesleff I., Kraal G., Tryggvason K.;  
RT "Cloning of a novel bacteria-binding receptor structurally related to scavenger receptors and expressed in a subset of macrophages.";  
RL Cell 80:603-609(1995).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99265975; PubMed=1031948;  
RA Kangas M., Brannstrom A., Elomaa O., Matsuda Y., Eddy R., Shows T.B., Tryggvason K.;  
RT "Structure and chromosomal localization of the human and murine genes for the macrophage MARCO receptor.";  
RL Genomics 38:82-89(1999).  
CC -!- FUNCTION: Bind Gram-positive and Gram-negative bacteria.  
CC -!- SUBCELLULAR LOCATION: Type II membrane protein (Probable).  
CC -!- TISSUE SPECIFICITY: Expressed in subpopulations of macrophages in the spleen and the medullary cord of lymph nodes.  
CC -!- SIMILARITY: Contains 1 collagenous domain.  
CC -!- SIMILARITY: Contains 1 SRCR domain.  
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CC EMBL; AF100956; AAC69905.1; -  
CC EMBL; U16789; AAA67751.1; -  
CC EMBL; U16790; AAA67752.1; -  
CC EMBL; D38412; BAA18910.1; -  
CC EMBL; D84066; BAA12208.1; -  
CC MGD; MGI:88447; Coll1a2.  
CC InterPro; IPR008161; Clg\_helix.  
CC InterPro; IPR008160; Collagen.  
CC InterPro; IPR008985; ConA-like\_lect.  
CC InterPro; IPR008885; Fib\_collagen\_C.  
CC InterPro; IPR001791; Laminin\_G.  
CC InterPro; IPR003129; TSPN.  
CC Pfam; PF01410; COLFI; 1.  
CC Pfam; PF01391; Collagen; 18.  
CC Pfam; PF02210; TSPN; 1.  
CC ProDom; PD000007; Clg\_helix; 1.  
CC ProDom; PD002078; Fib\_collagen\_C; 1.  
CC SMART; SM00038; COLFI; 1.  
CC SMART; SM00282; LamG; 1.  
CC SMART; SM00210; TSPN; 1.  
CC Extracellular matrix; Connective tissue; Repeat; Hydroxylation; Glycoprotein; Collagen; Alternative splicing; Signal.  
CC SIGNAL 1 22  
CC CHAIN 23 1500  
CC COLLAGEN ALPHA 2(XI) CHAIN.  
CC CARBOXYL-TERMINAL PROPEPTIDE.  
CC TSP N-TERMINAL.  
CC NONHELICAL REGION.  
CC TRIPLE-HELICAL REGION.  
CC NONHELICAL REGION.  
CC N-LINKED (GLCNAC...) (POTENTIAL).  
CC Missing (in isoform 3, isoform 5, isoform 6 and isoform 7).  
CC /FTIQ-VSP 007345.  
CC Missing (in isoform 2, isoform 4, isoform 5 and isoform 6).  
CC /FTIQ-VSP 007346.  
CC Missing (in isoform 4, isoform 6 and isoform 7).  
CC /FTIQ-VSP 007347.  
CC R -> L (IN REF. 2).  
CC P -> S (IN REF. 3).  
CC NO -> KP (IN REF. 2).  
CC V -> A (IN REF. 2).  
CC TGP -> S (IN REF. 2).  
CC A -> S (IN REF. 2).  
CC R -> G (IN REF. 2).  
CC G -> V (IN REF. 2).  
CC G -> D (IN REF. 2).  
CC E -> V (IN REF. 2).  
CC P -> S (IN REF. 2).  
CC A -> T (IN REF. 2).  
CC I -> M (IN REF. 2).  
CC SQ SEQUENCE 1736 AA; 171535 MW; 18D792DA3387C61 CRC64;

Query Match 46.2%; Score 182; DB 1; Length 1736;  
Best Local Similarity 50.0%; Pred. No. 1.6e-10;  
Matches 36; Conservative 8; Mismatches 28; Indels 0; Gaps 0;  
Cy 1 GPKGDDKEDPGEKHKVGMKGIKGLDMGRGNIGTKPTGKKGDKGKLL 60  
Db 1282 GPRGQDGAKDRGDEGPGQPGSGPGTGENPGPLGKRGPAFTGPGRQGRKAGDGP 1341  
Qy 61 GIPGKKGKAGTV 72  
Db 1342 GAVGAPKTKGPV 1353  
RESULT 6  
MTCO\_MOUSE STANDARD; PRT; 518 AA.  
ID MTCO\_MOUSE

AC Q60754;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Macrophage receptor MARCO (Macrophage receptor with collagenous structure).  
GN MARCO.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=95171455; PubMed=7867067;  
RA Elomaa O., Kangas M., Sahiberg C., Tuukkanen J., Sormunen R., Liakka A., Thesleff I., Kraal G., Tryggvason K.;  
RT "Cloning of a novel bacteria-binding receptor structurally related to scavenger receptors and expressed in a subset of macrophages.";  
RL Cell 80:603-609(1995).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99265975; PubMed=1031948;  
RA Kangas M., Brannstrom A., Elomaa O., Matsuda Y., Eddy R., Shows T.B., Tryggvason K.;  
RT "Structure and chromosomal localization of the human and murine genes for the macrophage MARCO receptor.";  
RL Genomics 38:82-89(1999).  
CC -!- FUNCTION: Bind Gram-positive and Gram-negative bacteria.  
CC -!- SUBCELLULAR LOCATION: Type II membrane protein (Probable).  
CC -!- TISSUE SPECIFICITY: Expressed in subpopulations of macrophages in the spleen and the medullary cord of lymph nodes.  
CC -!- SIMILARITY: Contains 1 collagenous domain.  
CC -!- SIMILARITY: Contains 1 SRCR domain.  
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CC EMBL; U18424; AAA69638.1; -  
CC EMBL; AF128423; AAD51136.1; -  
CC EMBL; AF127927; AAD51136.1; JOINED.  
CC EMBL; AF127928; AAD51136.1; JOINED.  
CC EMBL; AF128169; AAD51136.1; JOINED.  
CC EMBL; AF128170; AAD51136.1; JOINED.  
CC EMBL; AF128171; AAD51136.1; JOINED.  
CC EMBL; AF127601; AAD51136.1; JOINED.  
CC EMBL; AF127602; AAD51136.1; JOINED.  
CC EMBL; AF128419; AAD51136.1; JOINED.  
CC EMBL; AF128420; AAD51136.1; JOINED.  
CC EMBL; AF128421; AAD51136.1; JOINED.  
CC EMBL; AF128422; AAD51136.1; JOINED.  
CC PIR; A55840; A55840.  
CC MGD; MGI:1309998; Marco.  
CC InterPro; IPR008161; Clg\_helix.  
CC InterPro; IPR008160; Collagen.  
CC InterPro; IPR001190; Srcr\_receptor.  
CC Pfam; PF01391; Collagen; 5.  
CC Pfam; PF00530; SRCR; 1.  
CC PRINTS; PR00258; SPRACTRCPTR.  
CC ProDom; PD000007; Clg\_helix; 3.  
CC SMART; SM00202; SR; 1.  
CC PROSITE; PS00420; SRCR\_1; FALSE\_NEG.  
CC PROSITE; PS0287; SRCR\_2; 1.  
CC Collagen; Transmembrane; Receptor; Glycoprotein; Signal-anchor. CYTOPLASMIC (POTENTIAL).  
CC DOMAIN 1 48  
CC TRANSMEM 49 69  
CC SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN) (POTENTIAL).  
CC DOMAIN 70 518  
CC EXTRACELLULAR (POTENTIAL).  
CC COLLAGEN-LIKE.  
CC DOMAIN 149 418

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FT DOMAIN 423 518 SRCR.
FT DISULFID 446 507 BY SIMILARITY.
FT DISULFID 459 517 BY SIMILARITY.
FT DISULFID 487 497 BY SIMILARITY.
FT CARBOHYD 87 138 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 138 187 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 518 AA; 52730 MW; B09E7601EAC23637 CRC64;

Query Match 45.9%; Score 181; DB 1; Length 518;
Best Local Similarity 48.6%; Pred. No. 6.1e-11;
Matches 34; Conservative 10; Mismatches 26; Indels 0; Gaps 0;

QY 1 GPKGDDGKDPGEKHKVGMGPKGKIGELDMGRGNIGKTGPIGKKGDKGLL 60
DQ 192 GPGGPPSGSGEAGLOGLTGAPGKQAGATGAPRGEKSGKDGILGTGPKGEHGTGDKDGL 251
QY 61 GIPGEKKGAG 70
DQ 252 GLPGNKDGMG 261

RESULT 7
OTOL ONCKE STANDARD; PRT; 508 AA.
ID OTOL ONCKE STANDARD; PRT; 2944 AA.
AC P83371;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Otolin-1 precursor.
GN OTOL.
OS Oncorhynchus keta (Chum salmon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8016;
RN [1]
RP SEQUENCE FROM N.A., SEQUENCE OF 26-40 AND 452-482, FUNCTION, AND
RP TISSUE SPECIFICITY.
RX MEDLINE=21845944; PubMed=11856329;
RA Murayama E., Takagi Y., Ohira T., Davis J.G., Greene M.I.,
RA Nagasawa H.;
RT "Fish otolith contains a unique structural protein, otolin-1."
RL Eur. J. Biochem. 269:688-696(2002).
CC -!- FUNCTION: May be part of the internal framework of the otolith
CC where it may provide nucleation sites to facilitate
CC calcification.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Selectively expressed in the sacculus where it
CC is localised to the otolith, the gelatinous layer of the otolithic
CC membrane, and part of the transitional epithelium.
CC -!- PTM: N-glycosylated.
CC -!- SIMILARITY: Contains 1 collagenous domain.
CC -!- SIMILARITY: Contains 1 Clq domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AB067770; BAB84561.1; -.
CC GO; GO:0005576; C:extracellular; IDA.
CC GO; GO:0045299; P:otolith mineralization; NAS.
CC InterPro; IPR001073; Clq.
CC InterPro; IPR008161; Clq_helix.
CC InterPro; IPR008160; Collagen.
CC InterPro; IPR008983; TNF_like.
CC Pfam; PF00386; Clq; 1.
CC PRINTS; PF01391; Collagen; 4.
CC PRODOM; PD000007; COMPLEMENTC1Q.
CC ProDom; PD000007; Clq_helix; 1.
RN [5]
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DR PROSITE; PS01113; Clq; 1.
KW Collagen; Glycoprotein; Signal.
FT SIGNAL 1 25
FT CHAIN 26 508 OTOLIN-1.
FT DOMAIN 144 367 COLLAGEN-LIKE.
FT DOMAIN 369 505 Clq.
FT CARBOHYD 121 121 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 416 416 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 508 AA; 52138 MW; 90438799ACE3E9BE CRC64;

Query Match 45.8%; Score 180.5; DB 1; Length 508;
Best Local Similarity 48.1%; Pred. No. 6.7e-11;
Matches 37; Conservative 11; Mismatches 22; Indels 7; Gaps 2;

QY 1 GPKGDDGKGPDP-----GEEGKKGKVGMRMPKGKIGELDMGRGNIGKTGPIGKKGDX 54
DQ 231 GLKGLDGERGKPGWNGTQGEKGLKIGPAGPSGLTGPWGQNGQKGWGEK-PTGEKGEK 289
QY 55 GEKGLIGIPGEKKGAGT 71
DQ 290 GEAGLPGPGRGLVGT 306

RESULT 8
CAL7 HUMAN STANDARD; PRT; 2944 AA.
ID CAL7 HUMAN STANDARD; PRT; 2944 AA.
AC Q02388; Q14054; Q16507;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Collagen alpha 1(VII) chain precursor (Long-chain collagen) (LC
DE collagen).
GN COL7A1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94327588; PubMed=8051117;
RA Cristiano A.M., Greenspan D.S., Lee S., Utito J.;
RT "Cloning of human type VII collagen. Complete primary sequence of the
RT alpha 1(VII) chain and identification of intragenic polymorphisms."
RL J. Biol. Chem. 269:20256-20262(1994).
RN [2]
RP SEQUENCE OF 128-1493 FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=93338437; PubMed=1307247;
RA Cristiano A.M., Rosenbaum L.M., Chung-Honet L.C., Parente M.G.,
RA Woodley D.T., Pan T.C., Zhang R.Z., Chu M.-L., Burgeson R.E.,
RA Utito J.;
RT "The large non-collagenous domain (NC-1) of type VII collagen is
RT amino-terminal and chimeric. Homology to cartilage matrix protein,
RT the type III domains of fibronectin and the A domains of von
RT Willebrand factor."
RL Hum. Mol. Genet. 1:475-481(1992).
RN [3]
RP SEQUENCE OF 815-1439 FROM N.A.
RX MEDLINE=91334380; PubMed=1871109;
RA Parente M.G., Chung L.C., Rynaenen J., Woodley D.T., Wynn K.W.,
RA Bauer E.A., Mattei M.-G., Chu M.-L., Utito J.;
RT "Human type VII collagen: cDNA cloning and chromosomal mapping of the
RT gene."
RL Proc. Natl. Acad. Sci. U.S.A. 88:6931-6935(1991).
RN [4]
RP SEQUENCE OF 369-1255 FROM N.A.
RX MEDLINE=93107742; PubMed=1469284;
RA Gammon W.R., Abernethy M.L., Padilla K.M., Prisavanh P.S.,
RA Cook M.E., Wright J., Briggaman R.A., Hunt S.W. III;
RT "Noncollagenous (NC1) domain of collagen VII resembles multidomain
RT adhesion proteins involved in tissue-specific organization of
RT extracellular matrix."
RL J. Invest. Dermatol. 99:691-696(1992).
RN [5]
```

RP SEQUENCE OF 340-675 FROM N.A.  
RC TISSUE=Keratinocytes;  
RX MEDLINE=9221902; PubMed=1567409;  
RA Tanaka T., Takahashi K., Furukawa F., Imamura S.;  
RT "Molecular cloning and characterization of type VII collagen cDNA.";  
RL Biochem. Biophys. Res. Commun. 183:958-963(1992).  
RN [6]  
RP SEQUENCE OF 2395-2944 FROM N.A.  
RX MEDLINE=93271985; PubMed=8499916;  
RA Greenspan D.S.;  
RT "The carboxyl-terminal half of type VII collagen, including the non-collagenous NC-2 domain and the intron/exon organization of the corresponding region of the COL7A1 gene.";  
RL Hum. Mol. Genet. 2:273-278(1993).  
RN [7]  
RP SEQUENCE OF 1-87 FROM N.A.  
RX TISSUE=Placenta;  
RC MEDLINE=94375010; PubMed=8088784;  
RA Christiano A.M., Hoffman G.G., Chung-Honet L.C., Lee S., Cheng W.,  
RA Utito J., Greenspan D.S.;  
RT "Structural organization of the human type VII collagen gene (COL7A1), composed of more exons than any previously characterized gene.";  
RL Genomics 21:169-179(1994).  
RN [8]  
RP VARIANT EBSDC ARG-2034.  
RX MEDLINE=89227237; PubMed=2653224;  
RA Fine J.D., Johnson L., Wright T.;  
RT "Epidermolysis bullosa simplex superficialis. A new variant of epidermolysis bullosa characterized by subcorneal skin cleavage mimicking peeling skin syndrome.";  
RL Arch. Dermatol. 125:633-638(1989).  
RN [9]  
RP REVIEW ON DEB VARIANTS.  
RX MEDLINE=98041696; PubMed=9375848;  
RA Jaervakallio A., Pulkkinen L., Utito J.;  
RT "Molecular basis of dystrophic epidermolysis bullosa: mutations in the type VII collagen gene (COL7A1).";  
RL Hum. Mutat. 10:338-347(1997).  
RN [10]  
RP VARIANT DEB LYS-2798.  
RX MEDLINE=92291877; PubMed=8513326;  
RA Christiano A.M., Greenspan D.S., Hoffman G.G., Zhang X., Tamai Y.,  
RA Lin A.N., Dietz H.C., Hovnanian A., Utito J.;  
RT "A missense mutation in type VII collagen in two affected siblings with recessive dystrophic epidermolysis bullosa.";  
RL Nat. Genet. 4:62-66(1993).  
RN [11]  
RP VARIANT DEB SER-2040.  
RX MEDLINE=94224777; PubMed=8170945;  
RA Christiano A.M., Rymaenen M., Utito J.;  
RT "Dominant dystrophic epidermolysis bullosa: identification of a Gly--Ser substitution in the triple-helical domain of type VII collagen.";  
RL Proc. Natl. Acad. Sci. U.S.A. 91:3549-3553(1994).  
RN [12]  
RP VARIANT DEB CYS-2623.  
RX MEDLINE=96081220; PubMed=8541842;  
RA Christiano A.M., Lee J.Y.-Y., Chen W.J., Laforgia S., Utito J.;  
RT "Pretibial epidermolysis bullosa: genetic linkage to COL7A1 and identification of a glycine-to-cysteine substitution in the triple-helical domain of type VII collagen.";  
RL Hum. Mol. Genet. 4:1579-1583(1995).  
RN [13]  
RP VARIANT DEB ARG-2043.  
RX MEDLINE=95164985; PubMed=7861014;  
RA Christiano A.M., Morriconi A., Paradisi M., Angelo C., Mazzanti C.,  
RA Cavallieri R., Utito J.;  
RT "A glycine-to-arginine substitution in the triple-helical domain of type VII collagen in a family with dominant dystrophic epidermolysis bullosa.";  
RL J. Invest. Dermatol. 104:438-440(1995).  
RN [14]  
RP VARIANTS DEB.  
RX MEDLINE=96220218; PubMed=8644729;  
RA Christiano A.M., McGrath J.A., Tan K.C., Utito J.;  
RT "Glycine substitutions in the triple-helical region of type VII collagen result in a spectrum of dystrophic epidermolysis bullosa phenotypes and patterns of inheritance.";  
RL Am. J. Hum. Genet. 58:671-681(1996).  
RN [15]  
RP VARIANT DEB ARG-2575.  
RX MEDLINE=96154068; PubMed=8592061;  
RA Shimizu H., McGrath J.A., Christiano A.M., Nishikawa T., Utito J.;  
RT "Molecular basis of recessive dystrophic epidermolysis bullosa: genotype/phenotype correlation in a case of moderate clinical severity.";  
RL J. Invest. Dermatol. 106:119-124(1996).  
RN [16]  
RP VARIANT DEB ARG-1782.  
RX MEDLINE=96183562; PubMed=8618018;  
RA Christiano A.M., McGrath J.A., Utito J.;  
RT "Influence of the second COL7A1 mutation in determining the phenotypic severity of recessive dystrophic epidermolysis bullosa.";  
RL J. Invest. Dermatol. 106:766-770(1996).  
RN [17]  
RP VARIANT DEB ASP-2073.  
RX MEDLINE=96310789; PubMed=8757758;  
RA Dunnill M.G.S., McGrath J.A., Richards A.J., Christiano A.M.,  
RA Utito J., Pope F.M., Eady R.A.J.;  
RT "Clinicopathological correlations of compound heterozygous COL7A1 mutations in recessive dystrophic epidermolysis bullosa.";  
RL J. Invest. Dermatol. 107:171-177(1996).  
RN [18]  
RP VARIANTS DEB TRP-1982; GLY-2008; ALA-2025; GLU-2049; TRP-2063 AND ARG-2575.  
RX MEDLINE=97465605; PubMed=9326325;  
RA Hovnanian A., Rochat A., Bodemer C., Petit E., Rivers C.A., Prost C.,  
RA Fraitag S., Christiano A.M., Utito J., Lathrop M., Barrandon Y.,  
RA de Prost Y.;  
RT "Characterization of 18 new mutations in COL7A1 in recessive dystrophic epidermolysis bullosa provides evidence for distinct molecular mechanisms underlying defective anchoring fibril formation.";  
RL Am. J. Hum. Genet. 61:599-610(1997).  
RN [19]  
RP VARIANT DEB ARG-1652.  
RX MEDLINE=98106792; PubMed=9444387;  
RA Cserhalmi-Friedman P.B., Karpatis S., Horvath A., Christiano A.M.;  
RT "Identification of a glycine substitution and a splice site mutation in the type VII collagen gene in a proband with mitis recessive dystrophic epidermolysis bullosa.";  
RL Arch. Dermatol. Res. 289:640-645(1997).  
RN [20]  
RP VARIANTS DEB ARG-2009 AND ARG-2043.  
RX MEDLINE=97358588; PubMed=9215684;  
RA Winberg J.-O., Hammami-Hausli N., Nilssen O., Anton-Lamprecht I.,  
RA Naylor S.L., Kerbacher K., Zimmermann M., Krajci P.,  
RA Gedde-Dahl T., Jr., Bruckner-Tuderman L.;  
RT "Modulation of disease severity of dystrophic epidermolysis bullosa by a splice site mutation in combination with a missense mutation in the COL7A1 gene.";  
RL Hum. Mol. Genet. 6:1125-1135(1997).  
RN [21]  
RP VARIANTS DEB ASP-1519; ASP-2006; GLU-2015 AND ARG-2034.  
RX MEDLINE=98334662; PubMed=9668111;  
RA Hammami-Hausli N., Schumann H., Raghunath M., Kilgus O., Luethi U.,  
RA Lager T., Bruckner-Tuderman L.;  
RT "Some, but not all, glycine substitution mutations in COL7A1 result in intracellular accumulation of collagen VII, loss of anchoring fibrils, and skin blistering.";  
RL J. Biol. Chem. 273:19228-19234(1998).  
RN [22]  
RP VARIANTS DEB CYS-2008; ARG-2207 AND SER-2775.  
RX MEDLINE=98410969; PubMed=9740253;  
RA Kon A., Pulkkinen L., Ishida-Yamamoto A., Hashimoto I., Utito J.;  
RT "Novel COL7A1 mutations in dystrophic forms of epidermolysis

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RT bullosa."
RL J. Invest. Dermatol. 111:534-537(1998).
RN [23]
RP VARIANT DB ARG-1347.
RX MEDLINE=90019477; PubMed=9804332;
RA Terracina M., Posteraro P., Schubert M., Sonogo G., Atzori F.,
Query Match 45.6%; Score 179.5; DB 1; Length 2944;
Best Local Similarity 43.4%; Pred. No. 4.6e-10;
Matches 36; Conservative 11; Mismatches 23; Indels 13; Gaps 1;
QY 1 GPKGDDEKGPGEKGKGVGMGKGIKGLGDMGDRGNIGKTPG----- 47
Db 1667 GPVGEKDGQDGDGDRGDRGSPGSGPKGDRGPGPGPGLVDTGPGAREKGEGDRGQ 1726
QY 48 IGKKGDKGEGKGLGIPGEGKAG 70
Db 1727 EGPRGPKGDPGLPGAGERGIEG 1749
RESULT 9
CA16 HUMAN
ID CA16 HUMAN STANDARD; FRT; 1028 AA.
AC P12109; O00117; O14040; Q14041; Q16258;
DT 01-OCT-1989 (Rel. 12, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Collagen alpha 1(VI) chain precursor.
GN COL6A1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=9005396; PubMed=2551669;
RA Chu M.-L., Pan T.-C., Conway D., Kuo H.-J., Glanville R.W., Timpl R.,
Mann K., Deutzmann R.;
RT "Sequence analysis of alpha 1(VI) and alpha 2(VI) chains of human type
VI collagen reveals internal triplication of globular domains similar
to the A domains of von Willebrand factor and two alpha 2(VI) chain
variants that differ in the carboxy terminus."
RL EMBO J. 8:1939-1946(1989).
RN [2]
RP SEQUENCE OF 144-268 AND 593-1028 FROM N.A.
RX MEDLINE=97262101; PubMed=9107679;
RA Trikka D., Davis T., Lapenta V., Brahe C., Kessling A.M.;
RT "Human COL6A1: Genomic characterization of the globular domains,
structural and evolutionary comparison with COL6A2."
RL Mamm. Genome 8:342-345(1997).
RN [3]
RP SEQUENCE OF 257-592 FROM N.A.
RX MEDLINE=89066644; PubMed=3198591;
RA Chu M.-L., Conway D., Pan T.-C., Baldwin C., Mann K., Deutzmann R.,
Timpl R.;
RT "Amino acid sequence of the triple-helical domain of human collagen
type VI."
RL J. Biol. Chem. 263:18601-18606(1988).
RN [4]
RP SEQUENCE OF 287-592 FROM N.A.
RX MEDLINE=92112205; PubMed=1765372;
RA Saitta B., Wang Y.-M., Renkart L., Zhang R.-Z., Pan T.-C., Timpl R.,
Chu M.-L.;
RT "The exon organization of the triple-helical coding regions of the
human alpha 1(VI) and alpha 2(VI) collagen genes is highly similar."
RL Genomics 11:145-153(1991).
RN [5]
RP SEQUENCE OF 422-492 FROM N.A.
RX MEDLINE=88029444; PubMed=365927;
RA Chu M.-L., Mann K., Deutzmann R., Pribula-Conway D.,
Hsu-Chen C.-C., Bernard M.P., Timpl R.;
RT "Characterization of three constituent chains of collagen type VI by
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RT peptide sequences and cDNA clones."
RL Eur. J. Biochem. 168:309-317(1987).
RN [6]
RP SEQUENCE OF 422-482 FROM N.A.
RX TISSUE=Placenta;
RA Weil D., Mattei M.-G., Passage E., N'Guyen V.C., Pribula-Conway D.,
Mann K., Deutzmann R., Timpl R., Chu M.-L.;
RT "Cloning and chromosomal localization of human genes encoding the
three chains of type VI collagen."
RL Am. J. Hum. Genet. 42:435-445(1988).
RN [7]
RP SEQUENCE OF 1-380 AND 383-1028 FROM N.A.
RX MEDLINE=94222059; PubMed=8168508;
RA Tillet E., Wiedemann H., Golbik R., Pan T.-C., Zhang R.-Z., Mann K.,
Chu M.-L., Timpl R.;
RT "Recombinant expression and structural and binding properties of
alpha 1(VI) and alpha 2(VI) chains of human collagen type VI."
RL Eur. J. Biochem. 221:177-185(1994).
RN [8]
RP VARIANT BM VAL-305.
RX MEDLINE=96376983; PubMed=8782832;
RA Joeblis G.J., Keizers H., Vreijling J.P., de Visser M., Speer M.C.,
Wolterman R.A., Baas F., Bohlhuis P.A.;
RT "Type VI collagen mutations in Bethlem myopathy, an autosomal dominant
myopathy with contractures."
RL Nat. Genet. 14:113-115(1996).
RN [9]
RP VARIANTS BM ARG-121 AND ASP-341.
RX MEDLINE=21853823; PubMed=11865138;
RA Scacheri P.C., Gillanders E.M., Subramony S.H., Vedanarayanan V.,
Crowe C.A., Thakore N., Bingler M., Hoffman E.P.;
RT "Novel mutations in collagen VI genes: expansion of the Bethlem
myopathy phenotype."
RL Neurology 58:593-602(2002).
CC -I- FUNCTION: Collagen VI acts as a cell-binding protein.
CC -I- SUBUNIT: Trimers composed of three different chains: alpha 1(VI),
alpha 2(VI), and alpha 3(VI).
CC -I- PTM: Prolines at the third position of the tripeptide repeating
unit (G-X-Y) are hydroxylated in some or all of the chains.
CC -I- DISEASE: Defects in COL6A1 are a cause of Bethlem myopathy (BM)
[MIM:158810]. BM is a rare autosomal dominant proximal myopathy
characterized by early childhood onset (complete penetrance by the
age of 5) and joint contractures most frequently affecting the
elbows and ankles.
CC -I- SIMILARITY: Contains 3 WFPA domains.
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or send an email to license@isb-sib.ch).
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EMBL; X15879; CAA33888.1; -
EMBL; X15880; CAA33889.1; -
EMBL; S75420; AAB20835.2; -
EMBL; S75385; AAB20835.2; JOINED.
EMBL; S75388; AAB20835.2; JOINED.
EMBL; S75390; AAB20835.2; JOINED.
EMBL; S75392; AAB20835.2; JOINED.
EMBL; S75394; AAB20835.2; JOINED.
EMBL; S75396; AAB20835.2; JOINED.
EMBL; S75398; AAB20835.2; JOINED.
EMBL; S75400; AAB20835.2; JOINED.
EMBL; S75402; AAB20835.2; JOINED.
EMBL; S75404; AAB20835.2; JOINED.
EMBL; S75406; AAB20835.2; JOINED.
EMBL; S75408; AAB20835.2; JOINED.
EMBL; S75410; AAB20835.2; JOINED.
EMBL; S75412; AAB20835.2; JOINED.
EMBL; S75414; AAB20835.2; JOINED.
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DR EMBL; S75416; AAB20835.2; JOINED.
DR EMBL; S75418; AAB20835.2; JOINED.
DR EMBL; X99109; CAA67559.1; -.
DR EMBL; X99135; CAA67576.1; -.
DR EMBL; X99136; CAA67576.1; JOINED.
DR EMBL; X06194; CAA29555.1; -.
DR EMBL; M20776; -. NOT ANNOTATED_CDS.
DR EMBL; M27447; AAB52055.1; -.
DR PIR; S05377; CGHUIA.
DR Genew; HGNC:2211; COL6A1.
DR MIM; 120220; -.
DR MIM; 158810; -.
DR GO; GO:000589; C:collagen type VI; NAS.
DR GO; GO:0007155; P:cell adhesion; NAS.
DR InterPro; IPR008161; Clg_helix.
DR InterPro; IPR008160; Collagen.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF00391; Collagen; 4.
DR Pfam; PF00392; vwa; 3.
DR PRINTS; PR00453; VWFADOMAIN.
DR PRODOM; PD000007; Clg_helix; 3.
DR SMART; SM00327; VWA; 3.
DR PROSITE; PS0234; VWEA; 3.
KW Extracellular matrix; Connective tissue; Repeat; Hydroxylation;
KW Glycoprotein; Collagen; Cell adhesion; Signal; Disease mutation.
FT SIGNAL 1 19
FT CHAIN 20 1028
FT DOMAIN 20 256
FT DOMAIN 257 592
FT DOMAIN 593 1028
FT DOMAIN 37 235
FT DOMAIN 615 805
FT DOMAIN 829 1021
FT SITE 262 264
FT SITE 442 444
FT SITE 478 480
FT CARBOHYD 212 212
FT CARBOHYD 516 516
FT CARBOHYD 537 537
FT CARBOHYD 804 804
FT CARBOHYD 896 896
FT VARIANT 121 121
FT VARIANT 305 305
FT VARIANT 341 341
FT CONFLICT 438 438
FT SEQUENCE 1028 AA; 108547 MW; 3D6CCD9A74146D0E CRC64;

Query Match
Best Local Similarity 44.0%; Score 179; DB 1; Length 1028;
Matches 37; Conservative 11; Mismatches 24; Indels 12; Gaps 2;

QY 1 GPKGDD---GSKGDFGEGKHGKVGVRGPKGKGELGDMGRGNIGKTPGKKGKDGKGB- 56
Db 389 GPGSGDEGAGPGPPGKGEAGDEGPNCPGCGERGPGGPRGTPGPRGPDGGEA 448
QY 57 -----KGLLGPGGKKGAGTV 72
Db 449 GPGQDQGREGPGVGVGDPGEAGPI 472

RESULT 10
COT7_HUMAN
ID COT7_HUMAN STANDARD; PRT; 289 AA.
AC Q9BXJ2.
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Complement-clg tumor necrosis factor-related protein 7 precursor.
GN ClQTNF7 OR CTRP7.
OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
[1]
RN NCBI_Taxid=9606;
RP SEQUENCE FROM N.A.
RA Piddington C.S., Sheppard P.O., Bishop P., Lasser G.W.;
RT "Homo sapiens complement-clq tumor necrosis factor-related protein.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBAJ databases.
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=22388257; PubMed=12477932;
RA Krausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Rahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -1- SIMILARITY: Contains 1 collagenous domain.
CC -1- SIMILARITY: Contains 1 Clq domain.
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CC EMBL; AF329839; AAK17963.1; -.
CC EMBL; BC022187; AAB22187.1; -.
CC EMBL; BC024015; AAB24015.1; -.
CC Genew; HGNC:14342; ClQTNF7.
CC InterPro; IPR001073; Clq.
CC InterPro; IPR008160; Collagen.
CC InterPro; IPR008983; TNF_like.
CC Pfam; PF00386; Clq; 1.
CC Pfam; PF01391; Collagen; 2.
CC PRINTS; PR00007; COMLEWNTClQ.
CC SMART; SM00110; ClQ; 1.
CC PROSITE; PS01113; Clq; 1.
CC Collagen; Signal.
KW SIGNAL 1 16
FT CHAIN 17 289
FT DOMAIN 38 139
FT DOMAIN 141 276
FT SEQUENCE 289 AA; 30683 MW; A61609FF86D26946 CRC64;

Query Match
Best Local Similarity 45.3%; Score 178.5; DB 1; Length 289;
Matches 36; Conservative 8; Mismatches 23; Indels 3; Gaps 1;

QY 1 GPKGDDGKGDPEGKHGKVGMRGPKGKGELGDMGRGNIGKTPGKKGKDGKGLL 60
Db 62 GRGDRGRGKGEKGEKGTAGLRGKTGTLGLAGE---KGDQGETGKKGPIGPEGKEGVGPI 118
QY 61 GIPGKEGKAG 70

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Db 119 GPGPKGDRG 128

## RESULT 11

CA1A\_CHICK STANDARD; PRT; 674 AA.  
ID P08125;  
DT 01-AUG-1988 (Rel. 08, Created)  
DT 01-NOV-1991 (Rel. 20, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Collagen alpha 1(X) chain precursor.  
GN COL10A1.  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE OF 48-674 FROM N.A., AND SEQUENCE OF 103-117 AND 453-466.  
RX MEDLINE=86168227; PubMed=3082876;  
RA Nimomiya Y., Gordon M., van der Rest M., Schmid T., Linsenmayer T.,  
Olsen B.R.;  
RT "The developmentally regulated type X collagen gene contains a long  
open reading frame without introns."  
RL J. Biol. Chem. 261:5041-5050(1986).  
RN [2]  
RP SEQUENCE OF 1-75 FROM N.A.  
RX MEDLINE=89054019; PubMed=2461368;  
RA Luvaille P., Nimomiya Y., Rosenblum N.D., Olsen B.R.;  
RT "The type X collagen gene. Intron sequences split the 5'-untranslated  
region and separate the coding regions for the non-collagenous amino-  
terminal and triple-helical domains."  
RL J. Biol. Chem. 263:18378-18385(1988).  
RN [3]  
RP REVISIONS TO C-TERMINUS.  
RX MEDLINE=89380199; PubMed=2476437;  
RA Yamaguchi N., Benva P.D., van der Rest M., Nimomiya Y.;  
RT "The cloning and sequencing of alpha 1(VIII) collagen cDNAs  
demonstrate that type VIII collagen is a short chain collagen and  
contains triple-helical and carboxyl-terminal non-triple-helical  
domains similar to those of type X collagen."  
RL J. Biol. Chem. 264:16022-16029(1989).  
CC -1- FUNCTION: Type X collagen is a product of hypertrophic  
chondrocytes and has been localized to presumptive  
mineralization zones of hyaline cartilage.  
CC -1- SUBUNIT: Homotrimer.  
CC -1- PM: Prolines at the third position of the tripeptide repeating  
unit (G-X-Y) are hydroxylated in some or all of the chains.  
CC -1- SIMILARITY: STRONG, TO ALPHA 1 AND 2 TYPE VIII COLLAGENS.  
CC -1- SIMILARITY: Contains 1 C1Q domain.  
CC -----  
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; M13496; AAA48736.1; ALT\_SEQ.  
DR EMBL; J04194; AAA48634.1; -.  
DR PIR; S23297; S23297.  
DR InterPro; IPR001073; C1q.  
DR InterPro; IPR008161; C1q helix.  
DR InterPro; IPR008160; Collagen.  
DR InterPro; IPR008983; TNF\_like.  
DR Pfam; PF00386; C1q; 1.  
DR Pfam; PF01391; Collagen; 8.  
DR PRINTS; PR00007; COMPLEMENTC1Q.  
DR ProDom; PD000007; C1q helix; 1.  
DR SMART; SM00110; C1q; 1.  
DR PROSITE; PS01113; C1Q; 1.  
KW Extracellular matrix; Connective tissue; Repeat; Hydroxylation;

KW Collagen; Signal.  
FT SIGNAL 1 18  
FT CHAIN 19 674  
FT DOMAIN 19 52  
FT DOMAIN 53 512  
FT DOMAIN 539 674  
FT DOMAIN 539 674  
FT MOD\_RES 453 453  
FT MOD\_RES 456 456  
SQ SEQUENCE 674 AA; 66434 MW; EAB48B1EF174B145 CRC64;  
  
Query Match 45.3%; Score 178.5; DB 1; Length 674;  
Best Local Similarity 49.4%; Pred. No. 1.4e-10;  
Matches 39; Conservative 8; Mismatches 23; Indels 9; Gaps 2;  
  
QY 1 GPKGDDGKGGPGEGKKGKVGKRMGPKGIK---CSFLGDMGDRGNIGKTGPIGKKGDKGK 57  
DB 313 GPKGDDGKGGPGEGKKGKVGKRMGPKGIK---CSFLGDMGDRGNIGKTGPIGKKGDKGK 57  
QY 58 GLLGI-----PGEKKGKAG 70  
DB 373 GLPGLDGKPGVPGEGQLPG 391  
  
RESULT 12  
CA21\_CHICK STANDARD; PRT; 1362 AA.  
ID CA21\_CHICK STANDARD; PRT; 1362 AA.  
AC P02467; P87491; P87492; Q90758; Q90792; Q90795; Q90797; Q92014;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Collagen alpha 2(I) chain precursor (Fragments).  
GN COL1A2.  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE OF 1-245; 262-448 AND 466-1362 FROM N.A.  
RX MEDLINE=86185168; PubMed=3868961;  
RA Boedtker H., Finer M., Aho S.;  
RT "The structure of the chicken alpha 2 collagen gene."  
RL Ann. N.Y. Acad. Sci. 460:85-116(1985).  
RN [2]  
RP SEQUENCE OF 1-89 FROM N.A.  
RX MEDLINE=89246518; PubMed=6135195;  
RA Tate V.E., Finer M.H., Boedtker H., Doty P.;  
RT "Chick pro alpha 2 (I) collagen gene: exon location and coding  
potential for the prepropeptide."  
RL Nucleic Acids Res. 11:91-104(1983).  
RN [3]  
RP SEQUENCE OF 1-14 FROM N.A.  
RX MEDLINE=82060240; PubMed=6946474;  
RA Vogeli G., Ohkubo H., Sobel M.E., Yamada Y., Pastan I.,  
de Crombrughe B.;  
RT "Structure of the promoter for chicken alpha 2 type I collagen gene."  
RL Proc. Natl. Acad. Sci. U.S.A. 78:5334-5338(1981).  
RN [4]  
RP SEQUENCE OF 1-33 FROM N.A.  
RX MEDLINE=84297217; PubMed=6473103;  
RA Aho S., Tate V.E., Boedtker H.;  
RT "Location of the 11 bp exon in the chicken pro alpha 2(I) collagen  
gene."  
RN [5]  
RP Nucleic Acids Res. 12:6117-6125(1984).  
RX SEQUENCE OF 1-79 FROM N.A.  
RX MEDLINE=88056316; PubMed=3678834;  
RA Finer M.H., Boedtker H., Doty P.;  
RT "Construction and characterization of cDNA clones encoding the 5' end  
of the chicken pro alpha 1(I) collagen mRNA."  
RL Gene 56:71-78(1987).  
RN [6]



RP SEQUENCE OF 78-92.  
RC TISSUE=Skin;  
RX MEDLINE=71115216; PubMed=5544653;  
RA Higberger J.H., Kang A.H., Gross J.;  
RT "Comparative studies on the amino acid sequence of the alpha 2-CB2  
RL peptides from chick and rat skin collagens.";  
RL Biochemistry 10:610-616(1971).  
RN [7]  
RP SEQUENCE OF 74-91; 263-448 AND 1088-1169 FROM N.A.  
RX MEDLINE=82058081; PubMed=6272119;  
RA Wozney J., Hanahan D., Tate V.E., Boedtker H., Doty P.;  
RT "Structure of the pro alpha 2 (I) collagen gene.";  
RL Nature 294:129-135(1991).  
RN [8]  
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RA Irani M., Pastan I., de Crombrughe B.;  
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RT amplification of a DNA segment containing an exon of 54 bp.";  
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CC -!- FUNCTION: Type I collagen is a member of group I collagen  
CC (fibrillar forming collagen).  
CC -!- SUBUNIT: Trimer of one alpha 2(I) and two alpha 1(I) chains.  
CC -!- TISSUE SPECIFICITY: Forms the fibrils of tendon, ligaments and  
CC bones. In bones the fibrils are mineralized with calcium  
CC hydroxyapatite.  
CC -!- PTM: Prolines at the third position of the tripeptide repeating  
CC unit (G-X-Y) are hydroxylated in some or all of the chains.  
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CC EMBL; M26300; AAA69962.1; JOINED.  
CC EMBL; M26301; AAA69962.1; JOINED.  
CC EMBL; M26302; AAA69962.1; JOINED.  
CC EMBL; M26303; AAA69962.1; JOINED.  
CC EMBL; M26304; AAA69962.1; JOINED.  
CC EMBL; M26305; AAA69962.1; JOINED.  
CC EMBL; M26306; AAA69962.1; JOINED.  
CC EMBL; M26307; AAA69962.1; JOINED.  
CC EMBL; M26308; AAA69962.1; JOINED.  
CC EMBL; M26309; AAA69962.1; JOINED.  
CC EMBL; M26310; AAA69962.1; JOINED.  
CC EMBL; M26311; AAA69962.1; JOINED.  
CC EMBL; M26312; AAA69962.1; JOINED.  
CC EMBL; M26313; AAA69962.1; JOINED.  
CC EMBL; M26314; AAA69962.1; JOINED.  
CC EMBL; M26315; AAA69962.1; JOINED.  
CC EMBL; M26316; AAA69962.1; JOINED.  
CC EMBL; M26317; AAA69962.1; JOINED.  
CC EMBL; M26318; AAA69962.1; JOINED.  
CC EMBL; M26319; AAA69962.1; JOINED.  
CC EMBL; M26320; AAA69962.1; JOINED.  
CC EMBL; M26321; AAA69962.1; JOINED.  
CC EMBL; M26322; AAA69962.1; JOINED.  
CC EMBL; M26323; AAA69962.1; JOINED.  
CC EMBL; M26324; AAA69962.1; JOINED.  
CC EMBL; M26325; AAA69962.1; JOINED.  
CC EMBL; M26326; AAA69962.1; JOINED.  
CC EMBL; M26327; AAA69962.1; JOINED.  
CC EMBL; M26328; AAA69962.1; JOINED.  
CC EMBL; M26329; AAA69962.1; JOINED.  
CC EMBL; M26330; AAA69962.1; JOINED.  
CC EMBL; M26331; AAA69962.1; JOINED.  
CC EMBL; M26332; AAA69962.1; JOINED.  
CC EMBL; M26333; AAA69962.1; JOINED.  
CC EMBL; M26334; AAA69962.1; JOINED.  
CC EMBL; M26335; AAA69962.1; JOINED.  
CC EMBL; M26336; AAA69962.1; JOINED.  
CC EMBL; M26337; AAA69962.1; JOINED.  
CC EMBL; M26338; AAA69962.1; JOINED.  
CC EMBL; M26339; AAA69962.1; JOINED.  
CC EMBL; M26340; AAA69962.1; JOINED.  
CC EMBL; M26341; AAA69962.1; JOINED.  
CC EMBL; M26342; AAA69962.1; JOINED.  
CC EMBL; M26343; AAA69962.1; JOINED.  
CC EMBL; M26344; AAA69962.1; JOINED.  
CC EMBL; M26345; AAA69962.1; JOINED.  
CC EMBL; M26346; AAA69962.1; JOINED.  
CC EMBL; M26347; AAA69962.1; JOINED.  
CC EMBL; M26348; AAA69962.1; JOINED.  
CC EMBL; M26349; AAA69962.1; JOINED.  
CC EMBL; M26350; AAA69962.1; JOINED.  
CC EMBL; M26351; AAA69962.1; JOINED.  
CC EMBL; M26352; AAA69962.1; JOINED.  
CC EMBL; M26353; AAA69962.1; JOINED.  
CC EMBL; M26354; AAA69962.1; JOINED.  
CC EMBL; M26355; AAA69962.1; JOINED.  
CC EMBL; M26356; AAA69962.1; JOINED.  
CC EMBL; M26357; AAA69962.1; JOINED.  
CC EMBL; M26358; AAA69962.1; JOINED.  
CC EMBL; M26359; AAA69962.1; JOINED.  
CC EMBL; M26360; AAA69962.1; JOINED.  
CC EMBL; M26361; AAA69962.1; JOINED.  
CC EMBL; M26362; AAA69962

```
DR InterPro; IPR008160; Collagen.
DR InterPro; IPR008885; Fib collagen C.
DR ProDom; PD000007; Clg helix; 4
DR ProDom; PD002078; Fib collagen_C; 1
DR SMART; SN00038; COLF1; 1
KW Extracellular matrix; Connective tissue; Repeat; Hydroxylation;
KW Glycoprotein; Collagen; Signal.

Query Match 45.1%; Score 177.5; DB 1; Length 1362;
Best Local Similarity 42.9%; Pred. No. 3.5e-10;
Matches 39; Conservative 8; Mismatches 23; Indels 21; Gaps 2;

QY 1 GPKDGEKDGDPGESEKHKVGMGPKIKYGLGMDGRNIGTKGPKGK----- 51
Db 557 GPSGPGAGEAGKPGERGLHGFVPGPGPRGRLPGESGAVGPAGTIGSRGSPGPPGD 616
QY 52 GDKGEXGLL-----GIPGKKGAG 70
Db 617 GNKGEGVNPAGAPCPAGPGGIPGPGVAG 647

RESULT 13
CA16 CHICK STANDARD; PRT; 1019 AA.
AC P20785;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Collagen alpha 1(VI) chain precursor.
GN COL6A1.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92241293; PubMed=1572359;
RA Walchli C., Koller E., Trueb J., Trueb B.;
RT "Structural comparison of the chicken genes for alpha 1(VI) and alpha
RT 2(VI) collagen."
RL Eur. J. Biochem. 205:583-589(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=89174602; PubMed=2784434;
RA Bonaldo P., Russo V., Bucciotti F., Bressan G.M., Colombatti A.;
RT "Alpha 1 chain of chick type VI collagen. The complete cDNA sequence
RT reveals a hybrid molecule made of one short collagen and three von
RT Willebrand factor type A-like domains."
RL J. Biol. Chem. 264:5575-5580(1989).
RN [3]
RP SEQUENCE OF 1-75 FROM N.A.
RX MEDLINE=93011107; PubMed=1396681;
RA Koller E., Trueb B.;
RT "Characterization of the chicken alpha 1(VI) collagen promoter."
RL Eur. J. Biochem. 208:769-774(1992).
CC -1- FUNCTION: Collagen VI acts as a cell-binding protein.
CC -1- SUBUNIT: trimers composed of three different chains: alpha 1(VI),
CC alpha 2(VI), and alpha 3(VI).
CC -1- PTM: Prolines at the third position of the tripeptide repeating
CC unit (G-X-Y) are hydroxylated in some or all of the chains.
CC -1- SIMILARITY: Contains 3 WFPA domains.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
DR EMBL; X64458; CAA41053.1; -.
DR EMBL; X57998; CAA41062.1; -.

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DR EMBL; J04598; AAB59954.1; -.
DR EMBL; X57987; CAA41053.1; -.
DR PIR; A32856; A32856. Clg helix.
DR InterPro; IPR008161; Clg helix.
DR InterPro; IPR008160; Collagen.
DR InterPro; IPR002035; VWF A.
DR Pfam; PF01391; Collagen; 6.
DR Pfam; PF00092; vwa; 3.
DR PRINTS; PR00453; VWFADOMAIN.
DR ProDom; PD000007; Clg helix; 3.
DR SMART; SM00327; VWA; 3.
DR PROSITE; PS02334; VWF A; 3.
KW Extracellular matrix; Connective tissue; Repeat; Hydroxylation;
KW Glycoprotein; Collagen; Cell adhesion; Signal.
FT SIGNAL 1 19
FT CHAIN 20 1019 COLLAGEN ALPHA 1(VI) CHAIN.
FT DOMAIN 37 233 WFPA 1.
FT DOMAIN 613 800 WFPA 2.
FT DOMAIN 854 1012 WFPA 3.
FT SITE 476 478 CELL ATTACHMENT SITE.
FT SITE 529 531 CELL ATTACHMENT SITE.
FT CARBOHYD 212 212 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 514 514 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 535 535 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 739 739 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 887 887 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 1019 AA; 107984 MW; 66B4C334B83BBA21 CRC64;

Query Match 44.8%; Score 176.5; DB 1; Length 1019;
Best Local Similarity 44.0%; Pred. No. 3.3e-10;
Matches 37; Conservative 8; Mismatches 24; Indels 15; Gaps 1;

QY 2 PKDGEKDGDPGESEKHK-----VGRMGPKGKIGELGMDGRNIGTKG 46
Db 253 PRGPPGPFDFGEGEGKPGLPQKGDAGDPGRPDGMGVGYQGMKDGKSGRSG 312
QY 47 PIKKGDKGKGLGIPGKKGAG 70
Db 313 AKGAKGKKGKIGIDGDMKGAG 336

RESULT 14
CA21 BOVIN STANDARD; PRT; 1364 AA.
ID CA21 BOVIN
AC P02465; O62649;
DT 21-JUL-1986 (Rel. 01, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Collagen alpha 2(I) chain precursor.
GN COL1A2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98290219; PubMed=9628255;
RA Shirai T., Hattori S., Sakaguchi M., Inouye S., Kimura A., Ebihara T.,
RA Irie S., Nagai Y., Horii H.;
RT "The complete cDNA coding sequence for the bovine proalpha2(I) chain
RT of type I procollagen."
RL Matrix Biol. 17:85-88(1998).
RN [2]
RP SEQUENCE OF 80-98.
RX TISSUE=Skin;
RX MEDLINE=75036115; PubMed=4609475;
RA Fietzek P.F., Breitkreutz D., Kuehn K.;
RT "Amino acid sequence of the amino-terminal region of calf skin
RT collagen."
RL Biochim. Biophys. Acta 365:305-310(1974).
RN [3]

```

Query Match 44.8%; Score 176.5; DB 1; Length 1364;  
Best Local Similarity 45.6%; Pred. No. 4.3e-10;

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CC -----
DR EMBL; D38162; BAA07367.1; -
DR EMBL; S74574; AAB33439.1; -
DR PIR; A55648; A55648.
DR MGI; MGI:88446; Coll1a1.
DR InterPro; IPR008161; Clg_helix.
DR InterPro; IPR008160; Collagen.
DR InterPro; IPR008985; ConA_like lec.gl.
DR InterPro; IPR000885; Fib_Collagen_C.
DR InterPro; IPR001791; Laminin_G.
DR InterPro; IPR003123; TSPN.
DR Pfam; PF01410; COLFI; 1.
DR Pfam; PF01391; Collagen; 16.
DR Pfam; PF02210; TSPN; 1.
DR ProDom; PD000007; Clg_helix; 4.
DR ProDom; PD002078; Fib_collagen_C; 1.
DR SMART; SM00038; COLFI; 1.
DR SMART; SM00282; LamG; 1.
DR SMART; SM00210; TSPN; 1.
KW Extracellular matrix; Connective tissue; Repeat; Hydroxylation;
KW Glycoprotein; Collagen; Signal; Alternative splicing;
KW Disease mutation.
FT SIGNAL 1 35
FT PROPEP 36 511
FT CHAIN 512 1561
FT PROPEP 1562 1804
FT DOMAIN 37 228
FT DOMAIN 229 417
FT DOMAIN 418 506
FT DOMAIN 507 509
FT DOMAIN 510 527
FT DOMAIN 528 1540
FT DOMAIN 1541 1561
FT CARBOHYD 1638 1638
FT SITE 610 610
FT SITE 1450 1450
FT VARSPLIC 329 413
FT VARIANT 189 195
FT VARIANT 196 1804
SQ SEQUENCE 1804 AA; 180963 MW; FE2DB9DEDE1E4219A CRC64;

POTENTIAL.
AMINO-TERMINAL PROPEPTIDE (POTENTIAL).
COLLAGEN ALPHA 1(XI) CHAIN.
CARBOXYL-TERMINAL PROPEPTIDE.
TSP N-TERMINAL.
NONHELICAL REGION.
TRIPLE-HELICAL REGION (INTERRUPTED).
SHORT NONHELICAL SEGMENT.
TELOPEPTIDE.
TRIPLE-HELICAL REGION.
NONHELICAL REGION (C-TERMINAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
CROSSLINKING.
CROSSLINKING.
Missing (in isoform short).
/FTId=VSP_001147.
LDERSRS -> SIEVRDR (IN CHONDRODYSPLASIA).
MISSING (IN CHONDRODYSPLASIA).
Query Match 44.8%; Score 176.5; DB 1; Length 1804;
Best Local Similarity 48.1%; Pred. No. 5.7e-10;
Matches 38; Conservative 5; Mismatches 27; Indels 9; Gaps 1;

Qy 1 GPKGDDGKGDGEGKHKVGR-----MGPKGIKGLGMGDRGNICKTGPIGKK 51
Db 1079 GPPGAPAGKAGPKGPGQAGRGVQGVGLPAGPAGSGEDGDKGEIGEPQKGSK 1138
Qy 52 GDKGEKGLLGIPEGKAG 70
Db 1139 GDKGENGPPGPGLOQPVG 1157
```

Search completed: March 8, 2004, 12:12:07  
Job time : 12.4185 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 8, 2004, 12:03:01 ; Search time 19.0308 Seconds  
(without alignments)  
363.925 Million cell updates/sec

Title: US-09-600-932-2\_COPY\_47\_118  
Perfect score: 394  
Sequence: 1 GPKGDDGKGDGPGEGKHGK.....DKGEKGLLGIPGKKGAGTV 72

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues  
Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 78:\*  
1: PIR1.\*  
2: PIR2.\*  
3: PIR3.\*  
4: PIR4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	342	86.8	277	JC7903	collectin liver 1
2	205	52.0	645	D90782	probable tail fiber
3	205	52.0	645	H85612	probable tail fiber
4	196	49.7	618	S22436	collagen alpha 2(I)
5	193	49.0	688	A53330	collagen alpha 2(I)
6	186.5	47.3	1775	A31893	collagen alpha 1(I)
7	184.5	46.8	1366	CGHU28	collagen alpha 2(I)
8	184.5	46.8	2551	B98047	hypothetical prote
9	183.5	46.6	291	T34494	type VII collagen
10	182	46.2	1549	I48103	macrophage bacteri
11	181	45.9	518	A55840	collagen alpha 2(I)
12	181	45.9	677	S23296	collagen alpha 1(X
13	180.5	45.8	674	S23297	hypothetical prote
14	180	45.7	181	T13518	collagen alpha 1(I
15	179.5	45.6	2944	A54849	collagen alpha 1(I
16	179	45.4	438	D90734	probable tail fiber
17	179	45.4	1028	1	CGHUIA
18	178.5	45.3	1027	S28774	collagen alpha 1(I
19	178	45.2	1146	A35857	collagen, cornea-s
20	177.5	45.1	888	S28791	collagen alpha 1(X
21	177	44.9	310	I50696	collagen alpha 1(I
22	176.5	44.8	1019	A32856	collagen alpha 1(I
23	176	44.7	547	A36046	collagen alpha 1(X
24	176	44.7	1532	A81262	collagen alpha 1(X
25	175.5	44.5	615	A05269	surfactant protein
26	174.5	44.3	374	A42046	pulmonary surfacta
27	174.5	44.3	375	A45225	collagen alpha 1(I
28	174.5	44.3	1025	S34839	collagen alpha 1(I
29	174	44.2	361	H90877	probable tail fiber

30	174	44.2	375	2	G85631	hypothetical prote
31	174	44.2	437	2	E90968	probable tail fiber
32	174	44.2	437	2	E90966	probable tail fiber
33	174	44.2	437	2	H90854	probable tail fiber
34	174	44.2	439	2	C90769	probable tail fiber
35	174	44.2	439	2	E85816	probable tail fiber
36	174	44.2	439	2	A85719	probable tail fiber
37	174	44.2	439	2	A85741	hypothetical prote
38	174	44.2	440	2	F85584	probable tail comp
39	174	44.2	920	2	A45748	collagen alpha 1(I
40	174	44.2	1869	1	CGHU4B	collagen alpha 1(I
41	174	44.2	1838	1	CGHUIV	collagen alpha 1(I
42	174	44.2	1843	2	S18803	collagen alpha 1(I
43	173.5	44.0	1496	1	CGHU2V	collagen alpha 2(I
44	173	43.9	358	2	T26281	hypothetical prote
45	173	43.9	1492	2	A40333	collagen alpha 1(I

ALIGNMENTS

RESULT 1  
JC7903  
collectin liver 1 - mouse  
C/Species: Mus musculus (house mouse)  
C/Date: 03-Feb-2003 #sequence\_revision 03-Feb-2003 #text\_change 31-Mar-2003  
C/Accession: JC7903  
R/Kawai, T.; Suzuki, Y.; Eda, S.; Kase, T.; Ohtani, K.; Sakai, Y.; Keshi, H.; Fukuh, A  
Biosci. Biotechnol. Biochem. 66, 2134-2145, 2002  
A/Title: Molecular cloning of mouse collectin liver 1.  
A/Reference number: JC7903; MUID:22333927; PMID:12450124  
A/Accession: JC7903  
A/Molecule type: mRNA  
A/Residues: 1-277 <KAW>  
A/Cross-references: DDBJ:AB016429  
A/Experimental source: liver  
C/Comment: This protein is a highly conserved cytosolic protein and belongs to a vertebr  
c development.  
C/Genetics:  
A/Gene: Cl11  
A/Map position: 15

Query Match 86.8%; Score 342; DB 2; Length 277;  
Best Local Similarity 86.1%; Pred. No. 2.4e-27;  
Matches 62; Conservative 5; Mismatches 5; Indels 0; Gaps 0;  
QY 1 GPKGDDGKGDGPGEGKHGKGVGMGPKGIKGLGDMGDRGNIGKTGPIGKKDKGKGLL 60  
DB 47 GPKGDDGGERGDTGEEGKGDKGVKVGQSGPKVVKGLGDMGAQGNIGKSGPIGKKDKGKGLL 106  
QY 61 GIPGKKGKAGTV 72  
DB 107 GIPGKKGKAGTI 118

RESULT 2  
D90782  
probable tail fiber protein [imported] - Escherichia coli (strain O157:H7, substrain R1  
C/Species: Escherichia coli  
C/Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 18-Jul-2001  
C/Accession: D90782  
R/Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.  
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shingawa, H.  
DNA Res. 8, 11-22, 2001  
A/Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gen  
A/Reference number: A99629; MUID:21156231; PMID:11259796  
A/Accession: D90782  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-645 <HAY>  
A/Cross-references: GB:BA000007; PIDN:BA834651.1; PID:gi3360688; GSPDB:GN00154  
A/Experimental source: strain O157:H7, substrain R1MD 0509952  
C/Genetics:

```
A;Gene: ECs1228
Query Match      52.0%; Score 205; DB 2; Length 645;
Best Local Similarity 54.3%; Pred. No. 3.3e-13;
Matches 38; Conservative 11; Mismatches 21; Indels 0; Gaps 0;

QY 1 GPKGDDGKGDGPGEGKKGKVRMPKIGKELGMDGRGNIGTKTIGKKGKGGKGLL 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 247 GPGGTGPKGDVGPKEGTGVPQPGPKGERGVDGAGVAPGPRGKGGQGERGPQ 306

QY 61 GIPGKKGKAG 70
    |||:|||||:
Db 307 GIPGLKGDGTG 316

RESULT 3
H85642
probable tail fiber protein Z1483 (similarity) - Escherichia coli (strain O157:H7, subsp
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 02-Nov-2001
C;Accession: H85642
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; PMID:21074935; PMID:11206551
A;Accession: H85642
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-645 <STO>
A;Cross-references: GB:AE005174; NID:G12514339; PIDN:AGS55604.1; GSPDB:GNO0145; UMGF:Z14
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: Z1483

Query Match      52.0%; Score 205; DB 2; Length 645;
Best Local Similarity 54.3%; Pred. No. 3.3e-13;
Matches 38; Conservative 11; Mismatches 21; Indels 0; Gaps 0;

QY 1 GPKGDDGKGDGPGEGKKGKVRMPKIGKELGMDGRGNIGTKTIGKKGKGGKGLL 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 247 GPGGTGPKGDVGPKEGTGVPQPGPKGERGVDGAGVAPGPRGKGGQGERGPQ 306

QY 61 GIPGKKGKAG 70
    |||:|||||:
Db 307 GIPGLKGDGTG 316

RESULT 4
S32436
collagen alpha 2(IX) chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 15-Sep-2003
C;Accession: S32436; S34487; S64673
R;Peraelae, M.; Haenninen, M.; Haestbacka, J.; Elima, K.; Vuorio, E.
FEBS Lett. 319, 177-180, 1993
A;Title: Molecular cloning of the human alpha-2(IX) collagen cDNA and assignment of the
A;Reference number: S32436; PMID:93202262; PMID:8454052
A;Accession: S32436
A;Molecule type: mRNA
A;Residues: 1-618 <PER1>
A;Cross-references: EMBL:M95610; NID:G1054872
R;Peraelae, M.; Haenninen, M.; Haestbacka, J.; Vuorio, E.
submitted to the EMBL Data Library, March 1993
A;Description: Molecular cloning of the human alpha-2 (IX) collagen cDNA and assignment
A;Reference number: S34487
A;Accession: S34487
A;Molecule type: mRNA
A;Residues: 1-26 'OT', 29 'S', 31-32 'LM', 35-561 'L', 563-578 'P', 580-618 <PER2>
A;Cross-references: EMBL:M95610; NID:G1054872
R;Diab, M.; Wu, J.J.; Eyre, D.R.
Biochem. J. 314, 327-332, 1996
A;Title: Collagen type IX from human cartilage: a structural profile of intermolecular d
```

```
A;Reference number: S64673; PMID:96195147; PMID:8660302
A;Accession: S64673
A;Molecule type: Protein
A;Residues: 123-133 'P', 135-137 <DIA>
A;Comment: Prolines and lysines at the third position of the tripeptide repeating unit
ed and subsequently O-glycosylated.
C;Genetics:
A;Gene: GDB:COL9A2
A;Cross-references: GDB:138310; OMIM:120260
A;Map position: 1p33-1p32.2
A;Complex: type IX collagen may be a heterotrimer of one alpha 1(IX) chain, one alpha 2
C;Function:
A;Description: structural component of extracellular fibrous polymer associated with ty
C;Keywords: chondroitin sulfate proteoglycan; coiled coil; extracellular matrix; glycop.
F;1-114/Domain: collagenous COL3 (fragment) #status predicted <NC3>
F;115-131/Domain: non-collagenous NC3 #status predicted <NC3>
F;132-470/Domain: collagenous COL2 #status predicted <COL2>
F;471-500/Domain: non-collagenous NC2 #status predicted <NC2>
F;501-615/Domain: collagenous COL1 #status predicted <COL1>
F;616-618/Domain: non-collagenous NC1 (fragment) #status predicted <NC1>
F;120/Binding site: chondroitin sulfate (Ser) (covalent) #status predicted

Query Match      49.7%; Score 196; DB 2; Length 618;
Best Local Similarity 51.4%; Pred. No. 2.6e-12;
Matches 36; Conservative 13; Mismatches 21; Indels 0; Gaps 0;

QY 1 GPKGDDGKGDGPGEGKKGKVRMPKIGKELGMDGRGNIGTKTIGKKGKGGKGLL 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 306 GPGGLPFGSPPPKGEFPPRGPRGIGQGQGGKGGKGGKGGKGGKGGKGGKGG 365

QY 61 GIPGKKGKAG 70
    |||:|||||:
Db 366 GIPGFGQLPG 375

RESULT 5
A53330
collagen alpha 2(IX) chain precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 15-Sep-2003
C;Accession: A53330; S22216
R;Peraelae, M.; Elima, K.; Metsaeranta, M.; Rosati, R.; de Crombrughe, B.; Vuorio, E.
J. Biol. Chem. 269, 5064-5071, 1994
A;Title: The exon structure of the mouse alpha2(IX) collagen gene shows unexpected dive
A;Reference number: A53330; PMID:94148964; PMID:8106484
A;Accession: A53330
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-688 <PER>
A;Cross-references: GB:Z22923; NID:G311949; PIDN:CAA80503.1; PID:G311950
R;Elima, K.; Metsaeranta, M.; Kallio, J.; Peraelae, M.; Herola, I.; Garofalo, S.; de Cr
Biochim. Biophys. Acta 1130, 78-80, 1992
A;Title: Specific hybridization probes for mouse alpha-2(IX) and alpha-1(X) collagen mR
A;Reference number: S22215; PMID:92182017; PMID:1543751
A;Accession: S22216
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: S21-524, 'M', 526-609, 'R', 611-665, 'G', 667-668 <ELI>
A;Cross-references: EMBL:X63014; NID:G49810; PIDN:CAA44742.1; PID:G49811
A;Note: the authors translated the codon GAC for residue 526 as His and GGT for residue
C;Genetics:
A;Introns: 24/3; 49/3; 61/3; 82/3; 100/3; 112/3; 120/3; 138/3; 156/3; 172/3; 191/3; 209
/3; 534/1; 597/1; 623/1
C;Keywords: coiled coil; extracellular matrix; glycoprotein; heterotrimer; hydroxylisin

Query Match      49.0%; Score 193; DB 2; Length 688;
Best Local Similarity 45.1%; Pred. No. 5.7e-12;
Matches 37; Conservative 14; Mismatches 19; Indels 12; Gaps 1;

QY 1 GPKGDDGKGGKGGKGGKGGKGGKGGKGGKGGKGGKGGKGGKGGKGGKGGKGG 48
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 342 GTKGGPKGKGGKGGKGGKGGKGGKGGKGGKGGKGGKGGKGGKGGKGGKGG 401
```

QY 49 GKKGDKGKGLLGPBKGKAG 70  
||:|||||:|  
DB 402 GRGPGGEGPPGPGPGLPG 423

## RESULT 6

A31893  
collagen alpha 1(IV) chain precursor - fruit fly (*Drosophila melanogaster*)  
C:Species: *Drosophila melanogaster*  
C>Date: 21-May-1990 #sequence\_revision 21-May-1990 #text\_change 21-Jul-2000  
C:Accession: A31893; A26692; A19442; S00020  
R:Blumberg, B.; Mackrell, A.J.; Fessler, J.H.  
J. Biol. Chem. 263, 18328-18337, 1988  
A:Title: *Drosophila* basement membrane procollagen alpha-1(IV). II. Complete cDNA sequence  
A:Reference number: A31893; MUID:89054012; PMID:3142875  
A:Accession: A31893  
A:Molecule type: mRNA  
A:Residues: 1-1775 <BLU>  
A:Cross-references: EMBL:M23704; NID:g157029; PIDN:AAA28404.1; PID:g157030  
R:Blumberg, B.; Mackrell, A.J.; Olson, P.F.; Kurkinen, M.; Monson, J.M.; Natzle, J.E.; R  
J. Biol. Chem. 262, 5947-5950, 1987  
A:Title: Basement membrane procollagen IV and its specialized carboxyl domain are conserved  
A:Reference number: A26692; MUID:87194801; PMID:3106345  
A:Accession: A26692  
A:Molecule type: mRNA  
A:Residues: 1065-1775 <BLU2>  
A:Cross-references: EMBL:J02727  
R:Monson, J.M.; Natzle, J.; Friedman, J.; McCarthy, B.J.  
Proc. Natl. Acad. Sci. U.S.A. 79, 1761-1765, 1982  
A:Title: Expression and novel structure of a collagen gene in *Drosophila*.  
A:Reference number: A19442; MUID:82197577; PMID:6210912  
A:Accession: A19442  
A:Molecule type: DNA  
A:Residues: 762-947, 'S', 949-996, 'T', 998-1230 <MON>  
A:Cross-references: GB:J01074; EMBL:V00200; NID:g7736; PIDN:CAA23486.2; PID:gs777391  
R:Cecchini, J.P.; Knibbeler, B.; Mirre, C.; le Parco, Y.  
Eur. J. Biochem. 165, 587-593, 1987  
A:Title: Evidence for a type-IV-related collagen in *Drosophila melanogaster*. Evolutionary  
A:Reference number: S00020; MUID:87246644; PMID:3109906  
A:Accession: S00020  
A:Molecule type: DNA  
A:Residues: 1355-1356, 'K', 1358-1359, 'K', 1361-1372, 'I', 1374-1495, 'R', 1497-1506, 'RA', 1509,  
A:Cross-references: EMBL:M28334  
C:Genetics:  
A:Gene: FlyBase:CG25C  
A:Cross-references: FlyBase:PEgn0000299  
A:Introns: 7/2; 23/3; 339/3; 505/2; 989/1; 1312/1; 1689/3  
C:Superfamily: collagen alpha 1(IV) chain  
C:Keywords: basement membrane; cell binding; coiled coil; disulfide bond; duplication; e  
F:1-23/Domain: signal sequence #status predicted <SIG>  
F:24-1775/Product: collagen alpha 1(IV) chain #status predicted <MAT>  
F:55-67/Region: cell attachment (R-G-D) motif  
F:130-132/Region: cell attachment (R-G-D) motif  
F:238-240/Region: cell attachment (R-G-D) motif  
F:297-299/Region: cell attachment (R-G-D) motif  
F:892-894/Region: cell attachment (R-G-D) motif  
F:1075-1077/Region: cell attachment (R-G-D) motif  
F:1173-1175/Region: cell attachment (R-G-D) motif  
F:1225-1227/Region: cell attachment (R-G-D) motif  
F:1545-1775/Domain: carboxyl-terminal nonhelical, N1 #status predicted <NC1>  
F:1656-1775/Domain: repeat NC1 #status predicted <NC12>  
F:72/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F:570-573/Disulfide bonds: interchain #status predicted  
F:1611-1617, 1720-1727/Disulfide bonds: #status predicted

Query Match 47.3%; Score 186.5; DB 2; Length 1775;  
Best Local Similarity 46.8%; Pred. No. 6.4e-11;  
Matches 37; Conservative 10; Mismatches 23; Indels 9; Gaps 1;

QY 1 GPKGDGGE-----KGPGEKGKGVGRMGPKGKGLGDMGRGNIGKTGPIGKK 51  
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DB 295 GRGDMGQKGEGGLVVRKGEPGEGTGLDQKGEKGLPGGPGGRGQGNFGPPGSTGQK 354

QY 52 GDKGEKGLLGPBKGKAG 70  
||:|||||:|  
DB 355 GDRGEPGLGLPGNPGQKG 373

## RESULT 7

CGH2S  
collagen alpha 2(I) chain precursor - human  
N:Alternate names: procollagen alpha 2(I) chain  
C:Species: *Homo sapiens* (man)  
C>Date: 30-Jun-1989 #sequence\_revision 25-Aug-1995 #text\_change 21-Jul-2000  
C:Accession: A28500; S00824; S09176; I55311; A58111; A28472; A42165; A34405; A90567; I5  
9005; A02865  
R:de Wet, W.; Bernard, M.; Benson-Chanda, V.; Chu, M.L.; Dickson, L.; Weil, D.; Ramirez  
J. Biol. Chem. 262, 16032-16036, 1987  
A:Title: Organization of the human pro-alpha-2(I) collagen gene.  
A:Reference number: A28500; MUID:86058962; PMID:2824475  
A:Accession: A28500  
A:Molecule type: DNA; mRNA  
A:Residues: 1-248, 'N', 250-1366 <DEW>  
A:Cross-references: GB:J03464; NID:g179595; PIDN:AA859374.1; PID:g179596  
R:Kuvivaniemi, H.; Tromp, G.; Chu, M.L.; Prockop, D.J.  
Biochem. J. 252, 633-640, 1988  
A:Title: Structure of a full-length cDNA clone for the prepro-alpha-2(I) chain of human  
A:Reference number: S00824; MUID:88339824; PMID:3421913  
A:Accession: S00824  
A:Molecule type: mRNA  
A:Residues: 1-275, 'A', 277-332, 'V', 334-337, 'A', 339-482, 'A', 484-548, 'D', 550-765 <KU11>  
A:Cross-references: EMBL:X00724; NID:g30022; PIDN:CAA68709.1; PID:g30023  
R:Dickson, L.A.; de Wet, W.; di Liberto, M.; Weil, D.; Ramirez, F.  
Nucleic Acids Res. 13, 3427-3438, 1985  
A:Title: Analysis of the promoter region and the N-propeptide domain of the human proal  
A:Reference number: S09176; MUID:85242047; PMID:4011429  
A:Accession: S09176  
A:Molecule type: DNA  
A:Residues: 1-23, 33-58, 'P', 60-93 <DIC>  
A:Cross-references: EMBL:X02488; NID:g30098; PIDN:CAA26320.1; PID:g30099  
R:Weil, D.; D'Alessio, M.; Ramirez, F.; Eyre, D.R.  
J. Biol. Chem. 265, 16007-16011, 1990  
A:Title: Structural and functional characterization of a splicing mutation in the pro-a  
A:Reference number: I55311; MUID:90368825; PMID:2394758  
A:Accession: I55311  
A>Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 76-93 <WE11>  
A:Cross-references: GB:M35391; NID:g189684; PIDN:AAA60041.1; PID:g189685  
A:Accession: A58111  
A:Molecule type: protein  
A:Residues: 23-75, 94-96 <WE12>  
A:Note: mutant sequence from a patient with Ehlers-Danlos syndrome type VII  
R:Wirtz, M.K.; Glanville, R.W.; Steinmann, B.; Rao, V.H.; Hollister, D.W.  
J. Biol. Chem. 262, 16376-16385, 1987  
A:Title: Ehlers-Danlos syndrome type VII. Deletion of 18 amino acids comprising the N-1  
A:Reference number: A28472; MUID:88059013; PMID:3680255  
A:Accession: A28472  
A:Molecule type: protein  
A:Residues: 32-75, 94-111 <WIR>  
A:Note: mutant sequence of patient with Ehlers-Danlos syndrome type VIIB  
R:Chiodo, A.A.; Hockey, A.; Cole, W.G.  
J. Biol. Chem. 267, 6361-6369, 1992  
A:Title: A base substitution at the splice acceptor site of intron 5 of the COL1A2 gene  
s-Danlos syndrome type VII.  
A:Reference number: A42165; MUID:92210617; PMID:1556139  
A:Accession: A42165  
A:Molecule type: mRNA  
A:Residues: 50-126 <CHI>  
A:Note: parts of this sequence were determined by protein sequencing; a mutant sequence  
R:Weil, D.; D'Alessio, M.; Ramirez, F.; Steinmann, B.; Wirtz, M.K.; Glanville, R.W.; Ho  
J. Biol. Chem. 264, 16804-16809, 1989  
A:Title: Temperature-dependent expression of a collagen splicing defect in the fibroblas  
A:Reference number: A34405; MUID:89380311; PMID:2777808  
A:Accession: A34405

A;Status: not compared with conceptual translation  
A;Molecule type: mRNA  
A;Residues: 58-108 <WEI3>  
A;Cross-references: GB:J05049  
A;Note: the accession cited by the authors is not found in GenBank  
A;Note: parts of this sequence were determined by protein sequencing; a mutant having 93  
R;Click, E.M.; Bornstein, P.  
Biochemistry 9, 4699-4706, 1970  
A;Title: Isolation and characterization of the cyanogen bromide peptides from the alpha  
A;Reference number: A90567; MUID:71038625; PMID:5529814  
A;Accession: A90567  
A;Molecule type: protein  
A;Residues: 'Z', '81', 'B', '83-96', '417-447' <CLI>  
A;Note: the compositions of peptides CNBR1, CNBR2 were determined; evidence f  
P;Kuiyantiemi, H.; Sabol, C.; Tromp, G.; Sippola-Thiele, M.; Prockop, D.J.  
J. Biol. Chem. 263, 11407-11413, 1988  
A;Note: mutant sequence from a patient with osteogenesis imperfecta  
A;Title: A 19-base pair deletion in the pro-alpha 2(I) gene of type I procollagen that c  
is asymptomatic mother.  
A;Reference number: 155264; MUID:88298792; PMID:3403536  
A;Accession: 155264  
A;Status: translation not shown; translated from GB/EMBL/DBJ  
A;Molecule type: DNA; mRNA  
A;Residues: 145-197 <KUI2>  
A;Cross-references: GB:M21671; NID:9189521; PIDN:AA59994.1; PID:G553506  
A;Note: single base mutation in intron leads to abnormal splicing of mRNA  
R;Chipman, S.D.; Shapiro, J.R.; McKinstry, M.B.; Stover, M.L.; Branson, P.; Rowe, D.W.  
J. Bone Miner. Res. 7, 793-805, 1992  
A;Title: Expression of mutant alpha (II)-procollagen in osteoblast and fibroblast culture  
A;Reference number: 155485; MUID:92351816; PMID:1642148  
A;Accession: 155485  
A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 163-181, 200-213 <CH2>  
A;Cross-references: GB:S41099; NID:9252702; PIDN:AA22761.1; PID:G252703  
A;Note: mutant sequence from a patient with osteogenesis imperfecta type IV  
R;Worgan, P.H.; Jacobs, H.G.; Segrest, J.P.; Cunningham, L.W.  
J. Biol. Chem. 245, 5042-5048, 1970  
A;Title: Comparative study of glycopeptides derived from selected vertebrate collagens.  
A;Reference number: A92069; MUID:71001508; PMID:4319110  
A;Accession: B92069  
A;Molecule type: protein  
A;Residues: 175-180 <MOR>  
A;Experimental source: skin  
A;Note: attachment of 2-O-alpha-D-glucosyl-O-beta-D-galactose to 5-hydroxylysine  
R;Pietrek, P.P.; Furthmayr, H.; Kuehn, K.  
Eur. J. Biochem. 47, 257-261, 1974  
A;Title: Comparative sequence studies on alpha2-CB2 from calf, human, rabbit and pig-ski  
A;Reference number: A91224; MUID:75008198; PMID:4412529  
A;Accession: A91224  
A;Molecule type: protein  
A;Residues: 418-447 <FIE>  
R;Tromp, G.; Prockop, D.J.  
Proc. Natl. Acad. Sci. U.S.A. 85, 5254-5258, 1988  
A;Title: Single base mutation in the pro alpha 2(I) collagen gene that causes efficient  
A;Reference number: 159125; MUID:88276936; PMID:2839839  
A;Accession: 159125  
A;Status: translation not shown; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 520-573 <TRO>  
A;Cross-references: GB:M21353; NID:9180881; PIDN:AA52053.1; PID:G190882  
A;Note: single base mutation in intron leads to splicing out of exon 28  
R;Bernard, M.P.; Myers, J.C.; Chu, M.L.; Ramirez, F.; Eikenberry, E.F.; Prockop, D.J.  
Biochemistry 22, 1139-1145, 1983  
A;Title: Structure of a cDNA for the proalpha-2 chain of human type I procollagen. Compa  
A;Reference number: S09174; MUID:83178919; PMID:6687691  
A;Accession: S09174  
A;Molecule type: mRNA  
A;Residues: 623-742, 'A', 744-764, 'X', 766-827, 'A', 829-830, 'P', 832-836, 'P', 838-1097, 'L', 109  
A;Cross-references: GB:J00115; GB:V00503; NID:930123; PIDN:CAA23761.1; PID:G825646  
A;Experimental source: skin fibroblast cells  
R;Forlino, A.; Zolezzi, F.; Valli, M.; Pignatti, P.F.; Cetta, G.; Brunelli, P.C.; Mottes  
Hum. Mol. Genet. 3, 2201-2206, 1994  
A;Title: Severe (type III) osteogenesis imperfecta due to glycine substitutions in the  
A;Reference number: 154365; MUID:95187161; PMID:7881420  
A;Accession: 168663  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 663-675, 'V', 677, 'P', 679-742, 'A', 744-746 <FOR>  
A;Cross-references: GB:L47668; NID:G1009095; PIDN:AA59577.1; PID:G1009096  
R;Niyibizi, C.; Bonadio, J.; Byers, P.H.; Byre, D.R.  
J. Biol. Chem. 267, 23108-23112, 1992  
A;Title: Incorporation of type I collagen molecules that contain a mutant alpha 2(I) ch  
A;Reference number: 155369; MUID:93054637; PMID:1385413  
A;Accession: 155369  
A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 665-666, 'D', 668-670 <NIY>  
A;Cross-references: GB:L00613; NID:G180888; PIDN:AA59384.1; PID:G180889  
A;Note: mutant sequence from a patient with osteogenesis imperfecta  
R;Bachman, J.F.; Hannagan, M.; Chan, D.; Cole, W.G.  
Biochem. J. 276, 765-770, 1991  
A;Title: Characterization of a type I collagen alpha 2(I) glycine-586 to valine substit  
e method.  
A;Reference number: A56799; MUID:91291136; PMID:2064612  
A;Accession: A56799  
A;Molecule type: mRNA  
A;Residues: 672-675, 'V', 677, 'P', 679-681 <BAT>  
A;Cross-references: GB:S39878; NID:G1679911; PIDN:AA19314.1; PID:G232761  
A;Note: sequence extracted from NCBI backbone (NCBI:39878, NCBI:39886)  
A;Note: mutant sequence of patient with osteogenesis imperfecta type IV; the authors su  
nrol sequence  
R;Maekelae, J.K.; Vuorio, T.; Vuorio, E.  
Biochim. Biophys. Acta 1049, 171-176, 1990  
A;Title: Growth-dependent modulation of type I collagen production and mRNA levels in c  
A;Reference number: S10768; MUID:90304220; PMID:2364107  
A;Accession: S10768  
A;Molecule type: mRNA  
A;Residues: 960-1021, 'L', 1023-1188, 'D', 1190-1197, 'S', 1199-1356 <MAE>  
A;Cross-references: EMBL:X55525; NID:G30101; PIDN:CAA39142.1; PID:G30102  
A;Experimental source: fibroblast cell culture  
R;Myers, J.C.; Chu, M.L.; Faro, S.H.; Clark, W.J.; Prockop, D.J.; Ramirez, F.  
Proc. Natl. Acad. Sci. U.S.A. 78, 3516-3520, 1981  
A;Title: Cloning a cDNA for the pro-alpha2 chain of human type I collagen.  
A;Reference number: A18855; MUID:81273090; PMID:6267597  
A;Accession: A18855  
A;Molecule type: mRNA  
A;Residues: 964-979, 'V', 981-1018, 'Q', 1020 <MYE>  
A;Cross-references: GB:J00114; NID:G180393; PIDN:AA51996.1; PID:G180394  
A;Note: 1019-Leu was also found  
R;Wenstrup, R.J.; Cohn, D.H.; Cohen, T.; Byers, P.H.  
J. Biol. Chem. 263, 7734-7740, 1988  
A;Title: Arginine for glycine substitution in the triple-helical domain of the products  
A;Reference number: 155285; MUID:88227975; PMID:2897363  
A;Accession: 155285  
A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1090-1107 <WEN1>  
A;Cross-references: GB:M22816; NID:G179602; PIDN:AA51844.1; PID:G179603  
A;Accession: 170059  
A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1090-1101, 'R', 1103-1107 <WEN2>  
A;Cross-references: GB:M22817; NID:G179606; PIDN:AA51846.1; PID:G179607  
A;Note: mutant sequence from a patient with osteogenesis imperfecta type IV  
R;Myers, J.C.; Dickson, L.A.; de Wet, W.O.; Bernard, M.P.; Chu, M.L.; di Liberto, M.; P  
J. Biol. Chem. 258, 10128-10135, 1983  
A;Title: Analysis of the 3' end of the human pro-alpha-2(I) collagen gene. Utilization  
A;Reference number: S09175; MUID:83290853; PMID:6309769  
A;Accession: S09175  
A;Molecule type: DNA  
Query Match 46.8%; Score 184.5; DB 1; Length 1366;  
Best Local Similarity 42.9%; Pred. No. 7.9e-11;  
Matches 39; Conservative 9; Mismatches 22; Indels 21; Gaps 2;



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QY   1 GPKGDDGEKDPGBEGKHKGVRMGPKIKEIGLDMGDGRNIGKTGPIGKK----- 51
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Db    559 GPSGFAGEVCKPBGRLHGFGLFGFAPRGERGGPPGESGAAGTGTGISRGFSGPGPD 618
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QY    52 GDKGEKGLL-----GIPEKKGKAG 70
      :||||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db    619 GNKGEPGVVGAVCTAGSPSGSLPFERGAAG 649
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RESULT 8  
B98047  
hypothetical protein sprl1403 [imported] - Streptococcus pneumoniae (strain R6)  
C;Species: Streptococcus pneumoniae  
C;Date: 22-Oct-2001 #sequence\_revision 22-Oct-2001 #text\_change 22-Oct-2001  
C;Accession: B98047  
E;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; Dehoff, B.S.;  
k, P.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M.  
J. Y. F. Sun, P.M.; Winkler, M.E.  
Y. J. Bacteriol. 183, 5709-5717, 2001  
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;  
A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.  
A;Reference number: A97872; PMID:21429245; PMID:11544234  
A;Accession: B98047  
A>Status: preliminary  
A:Molecule type: DNA  
A;Residues: 1-2551 <XUR>  
A;Cross-references: GB:AEO07317; PID:N.AL00207.1; PID:g15459054; GSFPDB:GN00174  
C;Genetics:  
A;Gene: spr1403

Query Match            46.6%; Score 184.5; DB 2; Length 2551;  
Best Local Similarity 52.9%; Pred. No. 1.4e-10;  
Matches 37; Conservative 8; Mismatches 22; Indels 3; Gaps 1;

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QY   1 GPKGDDDEKDPGEEGHKHKGVRMGPKIIZEIGLDMGDGRNIGKTGPIGKHGDKGEKGLL 60
      |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db    1251 GPXGXDGADCAKGEKAQGERRGTGAQGVVKEKDQGER---GLTSKGEKEDQGERGLT 1307
      |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY    61 GIPEKKGKAG 70
      |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db    1308 GAQAAGKDXG 1317
      |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||
```

RESULT 9  
T34494  
hypothetical protein JK1248.2 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 15-Sep-2003  
C;Accession: T34494  
K;Latreille, P.  
submitted to The EMBL Data Library, June 1995  
A;Description: The sequence of C. elegans cosmid JK1248.  
A;Reference number: Z21534  
A;Accession: T34494  
A>Status: preliminary; translated from GB/EMBL/DDBB  
A:Molecule type: DNA  
A;Residues: 1-291 <LAT>  
A;Cross-references: EMU:L.U29244; PID:AACT1083.1; GSFPDB:GN00020; CBSP:ZK1248.2  
A;Experimental source: strain Bristol N2; clone JK1248  
C;Genetics:  
A;Gene: CBSP-ZK1248.2  
A;Map position: 2  
A;Introns: 9/3

Query Match            46.6%; Score 183.5; DB 2; Length 291;  
Best Local Similarity 45.8%; Pred. No. 2.3e-11;  
Matches 38; Conservative 10; Mismatches 22; Indels 13; Gaps 2;

```
QY   1 GPKGDDDEKDPGEEGHKHKGVRMGPKIIZEIGLDMGDGRNIGKT-----GFI 48
      |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db    183 GGCGEPEGSEGEDVHEH-QVQLPGPKISGPTGQPQQDQSQDQTGAQCIPGAPGERGPR 241
      |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY    49 GKXGDKGEKGLLGIPGEKKGAKGT 71
      |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||
```

Db 242 GDKDNGENGSAAGGEGPGT 264

RESULT 10  
I48103  
type VII collagen - Chinese hamster (fragment)  
C:Species: Cricetulus griseus (Chinese hamster)  
C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 15-Sep-2003  
C:Accession: I48103  
R:Greenspan, D.S.  
Hum. Mol. Genet. 2, 273-278, 1993  
A:Title: The carboxyl-terminal half of type VII collagen, including the non-collagenous  
A:Reference number: I48103; MUID:93271985; PMID:8499916  
A:Accession: I48103  
A:Status: preliminary; translated from GE/EMBL/DBDJB  
A:Molecule type: mRNA  
A:Residues: 1-1549 <RES>  
A:Cross-references: GB:L06863; NID:g388624; PIDN:AAA36968.1; PID:g388625  
F:I484-1536/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 46.2%; Score 182; DB 2; Length 1549;  
Best Local Similarity 33.3%; Pred. No. 1.6e-10;  
Matches 40; Conservative 11; Mismatches 21; Indels 48; Gaps 2;

Qy 1 GPKGDD-----GEKGDGSEGEKGVGRMPKGIKGLGDMGDRGNTGKTGPIKKG 52  
Db 1054 GKGDPTGTGPPRGERGEFDRGDEHPQEGRLGMPGSGRDRGEKGDTPAGLKG 1113  
Qy 53 DK-----GEKGLGIPGEKKGATV 72  
Db 1114 DKGDSAVIEGPGIRGAKGWBGRPRGIDDKGPRGDNPNPGDKSGEPGDKSGAGSI 1173

RESULT 11  
A55840  
macrophage bacteria-binding receptor MARCO - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 23-Mar-1995 #sequence\_revision 05-Apr-1995 #text\_change 05-Nov-1999  
C:Accession: A55840  
R:Elomaa, O.; Kangas, M.; Sahlberg, C.; Tuukkanen, J.; Sormunen, R.; Liakka, A.; Thele  
Cell 80, 603-609, 1995  
A:Title: Cloning of a novel bacteria-binding receptor structurally related to scavenger  
A:Reference number: A55840; MUID:95171455; PMID:7867067  
A:Accession: A55840  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-518 <ELO>  
A:Cross-references: GB:U18424; NID:g682722; PIDN:AAA68638.1; PID:g682723  
C:Superfamily: scavenger receptor cysteine-rich domain homology  
C:Keywords: transmembrane protein  
F:418-518/Domain: scavenger receptor cysteine-rich domain homology <SRC>

Query Match 45.9%; Score 181; DB 2; Length 518;  
Best Local Similarity 48.6%; Pred. No. 7.1e-11;  
Matches 34; Conservative 10; Mismatches 26; Indels 0; Gaps 0;

Qy 1 GPKGDDGEKGDPEEGKHGKGVGRMPKGIKGLGDMGDRGNIGTKTGPICKGDKGEKLL 60  
Db 192 GPQGPFGSGEASLGILGTGAPGQGTGAPGPRGEKSGKGDIGLTGPKEHGTGDKGDL 251

Qy 61 GIFGEKKGAG 70  
Db 252 GLPFGKGDWG 261

```

RESULT 12
S23296
collagen alpha 2(IX) chain precursor - chicken
C/Species: Gallus gallus (chicken)
C/Date: 22-Nov-1993 #sequence, revision 09-Mar-1996 #text change 15-Sep-2003
C/Accession: S23296; C34493; A29032; B28062; B28754; A18856; A28518; S23296
R/Nipponiwa, Y.; Castagnola, P.; Gerecke, D.; Gordon, M.K.; Jacenko, O.; Luvalle, P.; M...

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maguchi, N.; Olsen, B.R.  
in Extracellular Matrix Genes, Sandell L.J. and Boyd C.D., eds., pp.79-114, Academic Press, 1986.  
A;Title: The molecular biology of collagens with short triple-helical domains.  
A;Reference number: S22243  
A;Accession: S23296  
A;Status: not compared with conceptual translation  
A;Molecule type: DNA  
A;Residues: 1-677 <N1>  
R;Nishimura, I.; Muragaki, Y.; Olsen, B.R.  
J. Biol. Chem. 264, 20033-20041, 1989  
A;Title: Tissue-specific forms of type IX collagen-proteoglycan arise from the use of two promoters.  
A;Reference number: A34493; PMID:90062114; PMID:2584206  
A;Accession: C34493  
A;Molecule type: mRNA  
A;Residues: 1-174 <N1>  
A;Cross-references: EMBL:M28660; NID:9211625; PIDN:AAA46709.1; PID:9211626  
R;McCormick, D.; van der Rest, M.; Goodship, J.; Lozano, G.; Ninomiya, Y.; Olsen, B.R.  
Proc. Natl. Acad. Sci. U.S.A. 84, 4044-4048, 1987  
A;Title: Structure of the glycosaminoglycan domain in the type IX collagen-proteoglycan.  
A;Reference number: A29032; PMID:87231947; PMID:3473493  
A;Accession: A29032  
A;Molecule type: mRNA  
A;Residues: 120-195 <MCC>  
A;Cross-references: GB:M16715; NID:9211365; PIDN:AAA4644.1; PID:9555431  
A;Accession: E29032  
A;Molecule type: protein  
A;Residues: 147-165;170-180, 'X', 182-188 <MC2>  
R;Lozano, G.; Olsen, B.R.  
submitted to the EMBL Data Library, April 1990  
A;Reference number: S22062  
A;Accession: S22062  
A;Molecule type: DNA  
A;Residues: 401, 'RA', 404-631, 'D', 633-677 <LO1>  
R;Lozano, G.; Ninomiya, Y.; Thompson, H.; Olsen, B.R.  
Proc. Natl. Acad. Sci. U.S.A. 82, 4050-4054, 1985  
A;Title: A distinct class of vertebrate collagen genes encodes chicken type IX collagen  
A;Reference number: A94705; PMID:85216631; PMID:3858862  
A;Accession: E28754  
A;Molecule type: DNA  
A;Residues: 404-633;644-677 <LO2>  
A;Cross-references: EMBL:M11327  
A;Note: this sequence has been revised in reference S22062  
R;Ninomiya, Y.; van der Rest, M.; Mayne, R.; Lozano, G.; Olsen, B.R.  
Biochemistry 24, 4223-4229, 1985  
A;Title: Construction and characterization of cDNA encoding the alpha2 chain of chicken type IX collagen  
A;Reference number: A18856; PMID:86026268; PMID:2996593  
A;Accession: A18856  
A;Molecule type: mRNA  
A;Residues: 401, 'RA', 404-677 <N12>  
A;Accession: B18956  
A;Molecule type: protein  
A;Residues: 433-435, 'X', 437-450;542-562 <N13>  
R;Huber, S.; Winterhalter, K.H.; Vaughan, L.  
J. Biol. Chem. 263, 752-756, 1988  
A;Title: Isolation and sequence analysis of the glycosaminoglycan attachment site of type IX collagen  
A;Reference number: A28518; PMID:88087195; PMID:3335523  
A;Accession: A28518  
A;Molecule type: protein  
A;Residues: 156-159, 'X', 161-166, 'X', 168-173, 'X', 175-178 <HUB>  
R;van der Rest, M.; Mayne, R.  
J. Biol. Chem. 263, 1615-1618, 1988  
A;Title: Type IX collagen proteoglycan from cartilage is covalently cross-linked to type IX collagen  
A;Reference number: S23813; PMID:88115274; PMID:3123475  
A;Accession: S23813  
A;Molecule type: protein  
A;Residues: 170-180, 'X', 182-184 <VAN>  
A;Note: evidence for aldimine cross-linkage of 190-lys to collagen alpha 1(II) chain is provided by the structure of type IX collagen.  
Ann. N. Y. Acad. Sci. 460, 38-46, 1985  
A;Title: The structure of type IX collagen.  
A;Reference number: S22238; PMID:86185164; PMID:3868958  
A;Accession: S22238

A;Molecule type: protein  
A;Residues: 542-567 <MAY>  
C;Genetics:  
A;Introns: 427/3; 439/3; 454/3; 465/3; 514/3; 533/1; 596/1; 622/1  
C;Keywords: chondroitin sulfate proteoglycan; coiled coil; extracellular matrix; glycoprotein  
F;1-21/Domain: signal sequence #status predicted <SIG>  
F;22-677/Product: collagen alpha 2(XI) chain #status predicted <MAT>  
F;25-161/Domain: non-collagenous COL3 #status predicted <COL3>  
F;162-178/Domain: non-collagenous NC3 #status predicted <NC3>  
F;179-517/Domain: non-collagenous COL2 #status predicted <COL2>  
F;518-547/Domain: non-collagenous NC2 #status predicted <NC2>  
F;548-662/Domain: non-collagenous COL1 #status predicted <COL1>  
F;663-677/Domain: non-collagenous NC1 #status predicted <NC1>  
F;158-178/Modified site: 4-hydroxyproline (Pro) #status experimental  
F;167/Binding site: chondroitin sulfate (Ser) (covalent) #status experimental  
F;181/Modified site: 5-hydroxylysine (Lys) #status experimental  
F;181/Binding site: carbohydrate (Lys) (covalent) #status experimental  
F;190/Modified site: allylsine (Lys) #status predicted  
Query Match 45.9%; Score 181; DB 2; Length 677;  
Best Local Similarity 51.3%; Pred. No. 9.1e-11;  
Matches 39; Conservative 7; Mismatches 24; Indels 6; Gaps 2;  
QY 1 GPKGDCDEKGD---PGEKGKGVGRMGPKGIKGL--GDMGDRGNIGKTGPICKGDK 54  
DB 383 GLKGRGGRGVPVGPAGPGEAGSGPKGQGPPIGPQGLPGVKGDKSGPKTGPKGSTGDP 442  
QY 55 GEKGLLGIPGEKGRAG 70  
DB 443 GVHGLAGVKGEKGS 458  
RESULT 13  
S23297  
collagen alpha 1(X) chain precursor - chicken  
N;Alternate names: type X collagen  
C;Species: Gallus gallus (chicken)  
C;Date: 07-Oct-1994 #sequence revision 10-Nov-1995 #text\_change 13-Aug-1999  
C;Accession: S23297; A31896; S65594; S77711; I50218  
R;Ninomiya, Y.; Castagnola, P.; Gerecke, D.; Gordon, M.K.; Jacenko, O.; Luvalle, P.; Maguchi, N.; Olsen, B.R.  
in Extracellular Matrix Genes, Sandell L.J. and Boyd C.D., eds., pp.79-114, Academic Press, 1986.  
A;Title: The molecular biology of collagens with short triple-helical domains.  
A;Reference number: S22243  
A;Accession: S23297  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-674 <NIN>  
R;Luvalle, P.; Ninomiya, Y.; Rosenblum, N.D.; Olsen, B.R.  
J. Biol. Chem. 263, 18378-18385, 1988  
A;Title: The type X collagen gene. Introns sequences split the 5'-untranslated region and the 3'-untranslated region.  
A;Reference number: A31896; PMID:89054019; PMID:2461368  
A;Accession: A31896  
A;Molecule type: mRNA  
A;Residues: 1-75 <LUV>  
R;Ninomiya, Y.; Gordon, M.; van der Rest, M.; Schmid, T.; Linsemayer, T.; Olsen, B.R.  
J. Biol. Chem. 261, 5041-5050, 1986  
A;Title: The developmentally regulated type X collagen gene contains a long open reading frame.  
A;Reference number: I50218; PMID:86168227; PMID:3082876  
A;Accession: S65594  
A;Molecule type: DNA  
A;Residues: 77, '9', 'D', 11-12, 'E', 114-117;453-466 <NIN2>  
629, 'FOAVLSLISMTIKGSSCQIQPMWVIFPLNMFILISQVSLKSNIPITMS' <NIN1>  
A;Cross-references: EMBL:M13496; NID:9211699; PIDN:AAA48736.1; PID:9211700  
A;Accession: S77711  
A;Molecule type: protein  
A;Residues: 104-112, 'X', 114-117;453-466 <NIN2>  
C;Superfamily: collagen alpha 1(VIII) chain; complement C1q carboxyl-terminal homology  
C;Keywords: coiled coil; extracellular matrix; glycoprotein; homotrimer; hydroxyproline  
F;1-18/Domain: signal sequence #status predicted <SIG>  
F;547-673/Domain: complement C1q carboxyl-terminal homology <C1Q>  
F;453-456/Modified site: hydroxyproline (Pro) #status experimental  
F;611/Binding site: carbohydrate (Asn) (covalent) #status predicted

```
Query Match          45.8%; Score 180.5; DB 2; Length 674;
Best Local Similarity 49.4%; Pred. No. 1e-10;
Matches 39; Conservative 8; Mismatches 23; Indels 9; Gaps 2;

QY 1 GPKGDKGKDPGEGKHGKVRGMPGKIK---GELGDMGDRGNIGKTPGKKGKDGKSK 57
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 313 GPKGDKGKDPGEGKHGKVRGMPGKIK---GELGDMGDRGNIGKTPGKKGKDGKSK 57
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 58 GLGKI-----GPKGKAG 70
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 373 GLGGLDGGKPGVPGSGQLPG 391
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

RESULT 14
T13518
hypothetical protein 29 - Bacillus phage phi-105
C:Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 13-Aug-1999
R:Kobayashi, K.; Okamura, K.; Inoue, T.; Sato, T.; Kobayashi, Y.
Submitted to the EMBL Data Library, July 1998
A:Description: Complete nucleotide sequence of Bacillus subtilis phage phi-105.
A:Reference number: Z17688
A:Accession: T13518
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-181 <KOB>
A:Cross-references: EMBL:AB016282; NID:d1253051; PID:d1037622; PIDN:BAA36635.1

Query Match          45.7%; Score 180; DB 2; Length 181;
Best Local Similarity 45.8%; Pred. No. 3.3e-11;
Matches 33; Conservative 13; Mismatches 26; Indels 0; Gaps 0;

QY 1 GPKGDKGKDPGEGKHGKVRGMPGKIKGELGDMGDRGNIGKTPGKKGKDGKSKGLL 60
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 46 GPKGDKGKDKGKTPGEGKPGKPGKPGKPGKPGKPGKPGKPGKPGKPGKPGK 105
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 61 GIPGKKGKATV 72
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 106 GPKGDKGDPKAVI 117
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

RESULT 15
A54849
collagen alpha 1(VII) chain precursor - human
N:Alternate names: procollagen alpha 1(VII) chain
C:Species: Homo sapiens (man)
C:Date: 04-Nov-1994 #sequence_revision 04-Nov-1994 #text_change 15-Sep-2003
C:Accession: A54849; PH0844; S16316; I56328; A30296; I84686
R:Christiano, A.M.; Greenspan, D.S.; Lee, S.; Uitto, J.
J. Biol. Chem. 269, 20256-20262, 1994
A:Title: Cloning of human type VII collagen. Complete primary sequence of the alpha1(VII)
A:Reference number: A54849; MUID:94321588; PMID:8051117
A:Accession: A54849
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-2944 <CHR>
A:Cross-references: GB:L02870; NID:9987124; PIDN:AAA75438.1; PID:G987125
R:Tanaka, T.; Takahashi, K.; Furukawa, F.; Imanura, S.
Biochem. Biophys. Res. Commun. 193, 958-963, 1992
A:Title: Molecular cloning and characterization of type VII collagen cDNA.
A:Reference number: PH0844; MUID:92231902; PMID:1567409
A:Accession: PH0844
A:Molecule type: mRNA
A:Residues: 'EPR', 340-475, 'RALSTASHSTLCWRATWHPNCRGSHWTRACPCNRPASHRAARAG', 524-528, 'C',
A:Cross-references: DDBJ:D11152; DDBJ:D13694; NID:G453698; PIDN:BA02853.1; PID:G453699
A:Experimental source: keratinocyte
A:Note: the authors translated the codon ACC for residues 394 and 397 as Tyr
R:Porte, M.G.; Chung, L.C.; Ryyanen, J.; Woodley, D.T.; Wynn, K.C.; Bauer, E.A.; Mat
Proc. Natl. Acad. Sci. U.S.A. 88, 6931-6935, 1991
A:Title: Human type VII collagen: cDNA cloning and chromosomal mapping of the gene.
A:Reference number: S16316; MUID:91334380; PMID:1871109
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F;2625,2631/binding site: carbohydrate (Lys) (covalent) #status experimental  
F;2634,2802,2804/Disulfide bonds: interchain #status predicted

Query Match 45.6%; Score 179.5; DB 2; Length 2944;  
Best Local Similarity 43.4%; Pred. No. 5.3e-10;  
Matches 36; Conservative 11; Mismatches 23; Indels 13; Gaps 1;

QY 1 GPKGDDGKDPGSEKKGKVGKMGKGIKGLGDMGDRGNIGKTGP----- 47  
1667 GPVGEKGDQDPGEDGRNGSPGSSGPKGDRGEPPGPPGRLVDTGPGAREKGEFGDRGQ 1726

Db

QY 48 IGKKGDGKGLGIPGEKKGAG 70  
1727 EGPRGPKGDPGLPGAPGERGIEG 1749

Db

Search completed: March 8, 2004, 12:16:19  
Job time : 19.0308 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 8, 2004, 12:07:46 ; Search time 18.7137 seconds  
(without alignments)  
198.629 Million cell updates/sec

Title: US-09-600-932-2\_COPY\_47\_118

Perfect score: 394

Sequence: 1 GPKGDGEGKDPGEGKHGK.....DKGKGILLGTPGKGRAGTV 72

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.\*

- 1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep.\*
- 2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep.\*
- 3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep.\*
- 4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep.\*
- 5: /cgn2\_6/ptodata/2/iaa/PCPUS\_COMB.pep.\*
- 6: /cgn2\_6/ptodata/2/iaa/backfile1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	205	52.0	519	4	US-09-453-702B-265
2	184.5	46.8	1024	3	US-08-931-820-2
3	184.5	46.8	1366	3	US-08-963-825-19
4	184.5	46.8	1366	4	US-09-500-811-19
5	184.5	46.8	1366	4	US-09-570-573-19
6	184.5	46.8	1366	4	US-09-548-608-19
7	184.5	46.8	1366	4	US-09-585-887-10
8	184.5	46.8	1366	4	US-09-289-578-10
9	181	45.9	489	2	US-08-794-795-7
10	181	45.9	489	3	US-09-249-200-7
11	181	45.9	518	1	US-08-392-367B-2
12	181	45.9	518	3	US-08-893-467A-2
13	178.5	45.3	492	4	US-08-468-996-11
14	176	44.7	399	4	US-09-134-000C-6019
15	174.5	44.3	128	4	US-09-227-357-190
16	171	43.4	495	2	US-08-794-795-2
17	171	43.4	495	3	US-09-249-200-2
18	171	43.4	520	2	US-08-794-795-6
19	171	43.4	520	3	US-09-249-200-6
20	170.5	43.3	1017	4	US-08-468-996-10
21	170.5	43.3	1060	3	US-08-931-820-3
22	170.5	43.3	1418	3	US-08-963-825-20
23	170.5	43.3	1418	3	US-09-010-999-1
24	170.5	43.3	1418	4	US-09-500-811-20
25	170.5	43.3	1418	4	US-09-570-573-20
26	170.5	43.3	1418	4	US-09-548-608-20
27	170	43.1	186	4	US-09-366-009-6

28	170	43.1	186	4	US-08-809-156B-6
29	170	43.1	464	2	US-08-836-854-19
30	170	43.1	464	4	US-09-366-009-7
31	170	43.1	464	4	US-08-809-156B-7
32	170	43.1	489	4	US-09-366-009-8
33	170	43.1	489	4	US-08-809-156B-8
34	169.5	43.0	532	1	US-08-494-168-9
35	169.5	43.0	595	3	US-09-219-849-48
36	169.5	43.0	595	3	US-09-219-849-50
37	169.5	43.0	684	1	US-08-555-669-12
38	169.5	43.0	684	3	US-09-073-663-12
39	169.5	43.0	822	3	US-09-219-849-49
40	169	42.9	546	1	US-08-494-168-10
41	169	42.9	557	3	US-09-320-095-10
42	169	42.9	557	3	US-09-523-487-10
43	168.5	42.8	1057	3	US-08-931-820-1
44	168.5	42.8	1341	3	US-08-963-825-18
45	168.5	42.8	1341	4	US-09-500-811-18

ALIGNMENTS

RESULT 1  
US-09-453-702B-265  
; Sequence 265, Application US/09453702B  
; Patent No. 6365723  
; GENERAL INFORMATION:  
; APPLICANT: Blattner, Frederick R.  
; Burland, Valerie  
; Perna, Nicole T.  
; Plunkett, Guy  
; Welch, Rod

TITLE OF INVENTION: No. 6365723el Sequences of E. coli O157  
NUMBER OF SEQUENCES: 265  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Quarles & Brady  
STREET: 1 South Pinckney Street  
CITY: Madison  
STATE: WI  
COUNTRY: US  
ZIP: 53701-2113

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.44Mb storage  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Word Perfect 8.0

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/453,702B  
FILING DATE: 03-Dec-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/110,955  
FILING DATE: 04-DEC-1998

ATTORNEY/AGENT INFORMATION:  
NAME: Seay, Nicholas J.  
REGISTRATION NUMBER: 27386  
REFERENCE/DOCKET NUMBER: 960296.95017  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (608) 251-5000  
TELEFAX: (608) 251-9166

INFORMATION FOR SEQ ID NO: 265:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 519 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 265:

US-09-453-702B-265  
Query Match 52.0%; Score 205; DB 4; Length 519;  
Best Local Similarity 54.3%; Pred. No. 1.4e-16;

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Matches 38; Conservative 11; Mismatches 21; Indels 0; Gaps 0;
QY 1 GPKGDDGKDPGEGKGGKVGKGMGPKGKIGKGLGMDGRGNIGKTGPIGKKGKGLL 60
Db 247 GPOGETGPKGDPGKGETGPGVGPQGPAGPKGBRGDVGAGQAGVGPAGPRGKGQGERGPQ 306
QY 61 GIPGKKGKAG 70
Db 307 GIPGLKDDTG 316

RESULT 2
US-08-931-820-2
; Sequence 2, Application US/08931820
; Patent No. 6010863
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Assay for collagen degradation
; NUMBER OF SEQUENCES: 4
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION: 435
; APPLICATION NUMBER: US/08/931,820
; FILING DATE:
; PRIOR APPLICATION NUMBER: EP 96202596.1
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1024 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; TISSUE TYPE: Collagen type I
US-08-931-820-2
Query Match 46.8%; Score 184.5; DB 3; Length 1024;
Best Local Similarity 42.9%; Pred. No. 8.2e-14;
Matches 39; Conservative 9; Mismatches 22; Indels 21; Gaps 2;
QY 1 GPKGDDGKDPGEGKGGKVGKGMGPKGKIGKGLGMDGRGNIGKTGPIGKKGKGLL 51
Db 480 GPGSGPAGEVKGKGERGLHGEFGLPGPAGPRGGRGPPGSGAAGTGPISGRGSPGPPGD 539
QY 52 GPKGKGLL-----GIPGKKGKAG 70
Db 540 GNGKPGVGVGAVGTAGPSPGSGLPGERGAAG 570

RESULT 3
US-08-963-825-19
; Sequence 19, Application US/08963825
; Patent No. 610689
; GENERAL INFORMATION:
; APPLICANT: Qvist, Per
; APPLICANT: Bonde, Martin
; TITLE OF INVENTION: A Method for Assaying Collagen Fragments
; TITLE OF INVENTION: in Body Fluids, A Test Kit and Means for Carrying Out the
; TITLE OF INVENTION: Method and Use of the Method to Diagnose the Presence of
; TITLE OF INVENTION: Disorders Associated with the Metabolism of
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby PC
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
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; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/963,825
; FILING DATE:
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/187,319
; FILING DATE: 21-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Gogoris, Adda C
; REGISTRATION NUMBER: 29,714
; REFERENCE/DOCKET NUMBER: 4305/08701
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-527-7700
; TELEFAX: 212-753-6237
; TELEX: 236687
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1366 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
; CLONE: collagen alpha 2- type I
US-08-963-825-19
Query Match 46.8%; Score 184.5; DB 3; Length 1366;
Best Local Similarity 42.9%; Pred. No. 1.1e-13;
Matches 39; Conservative 9; Mismatches 22; Indels 21; Gaps 2;
QY 1 GPKGDDGKDPGEGKGGKVGKGMGPKGKIGKGLGMDGRGNIGKTGPIGKKGKGLL 51
Db 559 GPGSGPAGEVKGKGERGLHGEFGLPGPAGPRGGRGPPGSGAAGTGPISGRGSPGPPGD 618
QY 52 GPKGKGLL-----GIPGKKGKAG 70
Db 619 GNGKPGVGVGAVGTAGPSPGSGLPGERGAAG 649

RESULT 4
US-09-500-811-19
; Sequence 19, Application US/09500811
; Patent No. 632314
; GENERAL INFORMATION:
; APPLICANT: Qvist, Per
; APPLICANT: Bonde, Martin
; TITLE OF INVENTION: A Method for Assaying Collagen Fragments
; TITLE OF INVENTION: in Body Fluids, A Test Kit and Means for Carrying Out the
; TITLE OF INVENTION: Method and Use of the Method to Diagnose the Presence of
; TITLE OF INVENTION: Disorders Associated with the Metabolism of
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby PC
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: US/09/500,811
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA: 08/187,319
; APPLICATION NUMBER: 08/187,319
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Gogoris, Adda C
; REGISTRATION NUMBER: 29,714
; REFERENCE/DOCKET NUMBER: 4305/08701
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-527-7700
; TELEFAX: 212-753-6237
; TELEX: 236687
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1366 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
; CLONE: collagen alpha 2- type I
US-09-500-811-19

Query Match 46.8%; Score 184.5; DB 4; Length 1366;
Best Local Similarity 42.9%; Pred. No. 1.1e-13;
Matches 39; Conservative 9; Mismatches 22; Indels 21; Gaps 2;

QY 1 GPKGDDGKGDGPGEGKHGKVGMRGPKGKGLGMDGDRGNIGKTGPIGKK-----51
Db 559 GPSGPAGEVGKPGERGLHGFGLPGAPRGPRGERGPPGESGAAGPTGPIGSRGSPGPPGPD 618
QY 52 GDKGKGLL-----GIPGKKGKAG 70
Db 619 GNGKPGVVGAVGTAGPSGSPGLPGERGAAG 649

RESULT 5
US-09-570-573-19
; Sequence 19, Application US/09570573
; Patent No. 6342361
; GENERAL INFORMATION:
; APPLICANT: Qvist, Per
; APPLICANT: Bonde, Martin
; TITLE OF INVENTION: A Method for Assaying Collagen Fragments
; TITLE OF INVENTION: in Body Fluids, A Test Kit and Means for Carrying Out the
; TITLE OF INVENTION: Method and Use of the Method to Diagnose the Presence of
; TITLE OF INVENTION: Disorders Associated with the Metabolism of
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby PC
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/570,573
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/187,319
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Gogoris, Adda C
; REGISTRATION NUMBER: 29,714
; REFERENCE/DOCKET NUMBER: 4305/08701
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-527-7700
; TELEFAX: 212-753-6237
; TELEX: 236687
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1366 amino acids
; TYPE: amino acid

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```

; REFERENCE/DOCKET NUMBER: 4305/08701
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-527-7700
; TELEFAX: 212-753-6237
; TELEX: 236687
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1366 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
; CLONE: collagen alpha 2- type I
US-09-570-573-19

Query Match 46.8%; Score 184.5; DB 4; Length 1366;
Best Local Similarity 42.9%; Pred. No. 1.1e-13;
Matches 39; Conservative 9; Mismatches 22; Indels 21; Gaps 2;

QY 1 GPKGDDGKGDGPGEGKHGKVGMRGPKGKGLGMDGDRGNIGKTGPIGKK-----51
Db 559 GPSGPAGEVGKPGERGLHGFGLPGAPRGPRGERGPPGESGAAGPTGPIGSRGSPGPPGPD 618
QY 52 GDKGKGLL-----GIPGKKGKAG 70
Db 619 GNGKPGVVGAVGTAGPSGSPGLPGERGAAG 649

RESULT 6
US-09-548-608-19
; Sequence 19, Application US/09548608
; Patent No. 6355442
; GENERAL INFORMATION:
; APPLICANT: Qvist, Per
; APPLICANT: Bonde, Martin
; TITLE OF INVENTION: A Method for Assaying Collagen Fragments
; TITLE OF INVENTION: in Body Fluids, A Test Kit and Means for Carrying Out the
; TITLE OF INVENTION: Method and Use of the Method to Diagnose the Presence of
; TITLE OF INVENTION: Disorders Associated with the Metabolism of
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby PC
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/548,608
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/187,319
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Gogoris, Adda C
; REGISTRATION NUMBER: 29,714
; REFERENCE/DOCKET NUMBER: 4305/08701
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-527-7700
; TELEFAX: 212-753-6237
; TELEX: 236687
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1366 amino acids
; TYPE: amino acid

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; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
; CLONE: collagen alpha 2- type I
US-09-548-608-19

Query Match      46.8%; Score 184.5; DB 4; Length 1366;
Best Local Similarity 42.9%; Pred. No. 1.1e-13;
Matches 39; Conservative 9; Mismatches 22; Indels 21; Gaps 2;

QY 1 GPKGDDGKGDGEGKHGKVGKMGPKGKIGLGMGDRGNIGKTGPIGKK----- 51
Db 559 GPSGPAGEVKGPKGRLHGEFGLPGPAGPRGGRGPPGESGAAGTGPISGRGSPGPPGPD 618
QY 52 GDKGEGKLL-----GIPGKKGAG 70
Db 619 GNKGEPGVGAVGTAGPSGSLPGERGAAG 649

RESULT 7
US-09-585-887-10
; Sequence 10, Application US/09585887
; Patent No. 6413742
; GENERAL INFORMATION:
; APPLICANT: Olsen, David R
; APPLICANT: Chang, Robert
; APPLICANT: McMullin, Hugh
; APPLICANT: Hitzeman, Ronald A.
; APPLICANT: Chisholm, George
; TITLE OF INVENTION: NOVEL METHODS FOR THE PRODUCTION OF GELATIN AND
; TITLE OF INVENTION: FULL-LENGTH TRIPLE HELICAL COLLAGEN IN RECOMBINANT
; FILE REFERENCE: 225002030400
; CURRENT APPLICATION NUMBER: US/09/585,887
; CURRENT FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: 09/289,578
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/084,828
; PRIOR FILING DATE: 1998-05-08
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 10
; LENGTH: 1366
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-585-887-10

Query Match      46.8%; Score 184.5; DB 4; Length 1366;
Best Local Similarity 42.9%; Pred. No. 1.1e-13;
Matches 39; Conservative 9; Mismatches 22; Indels 21; Gaps 2;

QY 1 GPKGDDGKGDGEGKHGKVGKMGPKGKIGLGMGDRGNIGKTGPIGKK----- 51
Db 559 GPSGPAGEVKGPKGRLHGEFGLPGPAGPRGGRGPPGESGAAGTGPISGRGSPGPPGPD 618
QY 52 GDKGEGKLL-----GIPGKKGAG 70
Db 619 GNKGEPGVGAVGTAGPSGSLPGERGAAG 649

RESULT 8
US-09-585-887-10
; Sequence 10, Application US/09289578
; Patent No. 6428978
; GENERAL INFORMATION:
; APPLICANT: Olsen, David R
; APPLICANT: Chang, Robert
; APPLICANT: McMullin, Hugh
; APPLICANT: Hitzeman, Ronald A.
; APPLICANT: Chisholm, George
; TITLE OF INVENTION: NOVEL METHODS FOR THE PRODUCTION OF GELATIN AND
```

```
; TITLE OF INVENTION: FULL-LENGTH TRIPLE HELICAL COLLAGEN IN RECOMBINANT
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 225002030400
; CURRENT APPLICATION NUMBER: US/09/289,578
; CURRENT FILING DATE: 1999-04-10
; PRIOR APPLICATION NUMBER: 60/084,828
; PRIOR FILING DATE: 1998-05-08
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 10
; LENGTH: 1366
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-289-578-10

Query Match      46.8%; Score 184.5; DB 4; Length 1366;
Best Local Similarity 42.9%; Pred. No. 1.1e-13;
Matches 39; Conservative 9; Mismatches 22; Indels 21; Gaps 2;

QY 1 GPKGDDGKGDGEGKHGKVGKMGPKGKIGLGMGDRGNIGKTGPIGKK----- 51
Db 559 GPSGPAGEVKGPKGRLHGEFGLPGPAGPRGGRGPPGESGAAGTGPISGRGSPGPPGPD 618
QY 52 GDKGEGKLL-----GIPGKKGAG 70
Db 619 GNKGEPGVGAVGTAGPSGSLPGERGAAG 649

RESULT 9
US-08-794-795-7
; Sequence 7, Application US/08794795
; Patent No. 5916766
; GENERAL INFORMATION:
; APPLICANT: Elshourlagy, Nabil
; APPLICANT: Adamou, John
; APPLICANT: Gross, Mitchell
; APPLICANT: Lysko, Paul
; TITLE OF INVENTION: Human Macro Scavenger Rec
; TITLE OF INVENTION: eptor
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Smithkline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/794,795
; FILING DATE: 04-FEB-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: ATGS0009P
; FILING DATE: 22-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Han, William T
; REGISTRATION NUMBER: 34,344
; REFERENCE/DOCKET NUMBER: ATGS0009
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5219
; TELEFAX: 610-270-4026
; TELEX:
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 489 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
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: MOLECULE TYPE: protein
US-08-794-795-7

Query Match 45.9%; Score 181; DB 2; Length 489;
Best Local Similarity 48.6%; Pred. No. 9.2e-14;
Matches 34; Conservative 10; Mismatches 26; Indels 0; Gaps 0;

QY 1 GKPGDDGKGDGEGEKHKYGRVGPFGKIGELGDMGDRGNIGTKPTIGKKDKGKGLL 60
Db 163 GPGGPPGSGKAGLQGLTGAPGKQATGAPPRGKSGKDILGTGPKGEHGTGDKGDL 222

QY 61 GIPGEKGKAG 70
Db 223 GLPGNKGDWG 232

RESULT 10
US-09-249-200-7
; Sequence 7, Application US/09249200
; Patent No. 6197931
; GENERAL INFORMATION:
; APPLICANT: ELSHOURBAGY, NABIL
; APPLICANT: ADAMOU, JOHN
; APPLICANT: GROSS, MITCHELL
; APPLICANT: LYSKO, PAUL
; TITLE OF INVENTION: HUMAN MARCO SCAVENGER RECEPTOR
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ratner & Prestia
; STREET: P.O. Box 980
; CITY: Valley Forge
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/249,200
; FILING DATE: 12-FEB-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/794,795
; FILING DATE: 04-FEB-1997
; APPLICATION NUMBER: 60/017,699
; FILING DATE: 23-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Prestia, Paul F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: ATG-50009-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0700
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 489 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-249-200-7

Query Match 45.9%; Score 181; DB 3; Length 489;
Best Local Similarity 48.6%; Pred. No. 9.2e-14;
Matches 34; Conservative 10; Mismatches 26; Indels 0; Gaps 0;

QY 1 GKPGDDGKGDGEGEKHKYGRVGPFGKIGELGDMGDRGNIGTKPTIGKKDKGKGLL 60
Db 163 GPGGPPGSGKAGLQGLTGAPGKQATGAPPRGKSGKDILGTGPKGEHGTGDKGDL 222

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QY 61 GIPGEKKGAG 70
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Db 223 GLPGNGKGMG 232

RESULT 11
US-08-392-367B-2
; Sequence 2, Application US/08392367B
; Patent No. 5691197
; GENERAL INFORMATION:
; APPLICANT: Tryggevason, Karl
; APPLICANT: Elomaa, Outi
; APPLICANT: Kangas, Maarit
; TITLE OF INVENTION: An Insolated DNA Sequence For a
; Patent No. 5691197
; TITLE OF INVENTION: No. 5691197el Macrophage Receptor with
; TITLE OF INVENTION: a Collagenous Domain and the
; TITLE OF INVENTION: Polypeptide Chain Encoded by
; TITLE OF INVENTION: such a Sequence
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fay, Sharpe, Beall, Fagan,
; ADDRESSEE: Minnich & McKee
; STREET: 1100 Superior Avenue
; STREET: Suite 700
; CITY: Cleveland
; STATE: Ohio
; COUNTRY: U.S.A.
; ZIP: 44114-2518
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch,
; MEDIUM TYPE: 720 Kb storable
; COMPUTER: IBM PS/2, Model 35 SX
; OPERATING SYSTEM: DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/392,367B
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Minnich, Richard J.
; REGISTRATION NUMBER: 24,175
; REFERENCE/DOCKET NUMBER: TRV 2 009
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (216) 861-5582
; TELEFAX: (216) 241-1666
; TELEX: (216) 980162
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 518 amino acids
; TYPE: amino acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
US-08-392-367B-2

Query Match 45.9%; Score 181; DB 1; Length 518;
Best Local Similarity 48.6%; Pred. No. 9.8e-14;
Matches 34; Conservative 10; Mismatches 26; Indels 0; Gaps 0;

QY 1 GPKGDDCEKGPDEEGKHGKVGWGMGPKIGKELGDMGDRGNIGKTPGIGKXGDKGEKGLL 60
Db 192 GPQGPSPKSEAGLQGLTGAPGKQGTATGAPGRGRGKSGKGDILGTPKGEHGTGDKDKDL 251

QY 61 GIPGEKKGAG 70
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Db 252 GLPGNGKGMG 261

RESULT 12
US-08-893-467A-2
; Sequence 2, Application US/08893467A
; Patent No. 6063901
; GENERAL INFORMATION:

```

APPLICANT: Tytgvason, Karl  
APPLICANT: Elomaa, Outi  
APPLICANT: Kangas, Maarit  
TITLE OF INVENTION: An Insulated DNA Sequence For a  
Patent No. 6063901  
TITLE OF INVENTION: No. 6063901el Macrophage Receptor with  
TITLE OF INVENTION: A Collagenous Domain and the  
TITLE OF INVENTION: Polypeptide Chain Encoded by  
TITLE OF INVENTION: such a Sequence  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fay, Sharpe, Beall, Fagan,  
ADDRESSEE: Minnich & McKee  
STREET: 1100 Superior Avenue  
STREET: Suite 700  
CITY: Cleveland  
STATE: Ohio  
COUNTRY: U.S.A.  
ZIP: 44114-2518  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch,  
MEDIUM TYPE: 720 Kb storable  
COMPUTER: IBM PS/2, Model 35 SX  
OPERATING SYSTEM: DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/893,467A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Minnich, Richard J.  
REGISTRATION NUMBER: 24,175  
REFERENCE/DOCKET NUMBER: TRV 2 009  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (216) 861-5582  
TELEFAX: (216) 241-1666  
TELEX: (216) 980162  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 518 amino acids  
TYPE: amino acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
US-08-893-467A-2

Query Match 45.9%; Score 181; DB 3; Length 518;  
Best Local Similarity 48.6%; Pred. No. 9.8e-14;  
Matches 34; Conservative 10; Mismatches 26; Indels 0; Gaps 0;  
QY 1 GPKGDDGKGDPEEGKHGKVGKGMGPKGKIGKLGMDGRNIGKTGPIGKKGDKGKGLL 60  
DB 192 GPQGPSPKSGEAGLQGLTGAPKQKATGAPGPRGKSGKDGILGTGPKGHEGTKGDKGDL 251  
QY 61 GIPGKKGKAG 70  
DB 252 GLPGNKGDMG 261

RESULT 13  
US-08-468-996-11  
Sequence 11, Application US/08468996  
Patent No. 6645504  
GENERAL INFORMATION:  
APPLICANT: Weiner, Howard  
APPLICANT: Miller, Ariel  
APPLICANT: Zheng, Zheng  
APPLICANT: Ahmad, Al-Sabbagh  
TITLE OF INVENTION: BYSTANDER SUPPRESSION OF TYPE 1 DIABETES BY ORAL ADMINISTRATION OF  
TITLE OF INVENTION: GLUCAGON  
FILE REFERENCE: 1010/16959-US3  
CURRENT APPLICATION NUMBER: US/08/468,996  
CURRENT FILING DATE: 2003-02-07  
PRIOR APPLICATION NUMBER: US 07/843,752

PRIOR FILING DATE: 1992-02-28  
PRIOR APPLICATION NUMBER: US 07/460,852  
PRIOR FILING DATE: 1990-02-21  
PRIOR APPLICATION NUMBER: US 07/596,936  
PRIOR FILING DATE: 1990-10-15  
PRIOR APPLICATION NUMBER: US 07/065,734  
PRIOR FILING DATE: 1987-06-24  
PRIOR APPLICATION NUMBER: US 07/454,486  
PRIOR FILING DATE: 1989-12-20  
PRIOR APPLICATION NUMBER: US 07/487,732  
PRIOR FILING DATE: 1990-03-02  
PRIOR APPLICATION NUMBER: US 07/551,632  
PRIOR FILING DATE: 1990-07-10  
PRIOR APPLICATION NUMBER: US 07/379,778  
PRIOR FILING DATE: 1989-07-14  
PRIOR APPLICATION NUMBER: US 07/607,826  
PRIOR FILING DATE: 1990-10-31  
PRIOR APPLICATION NUMBER: US 07/595,468  
PRIOR FILING DATE: 1990-10-10  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: Patent in version 3.1  
SEQ ID NO 11  
LENGTH: 492  
TYPE: PRT  
ORGANISM: Bos taurus  
US-08-468-996-11

Query Match 45.3%; Score 178.5; DB 4; Length 492;  
Best Local Similarity 50.7%; Pred. No. 1.8e-13;  
Matches 37; Conservative 7; Mismatches 26; Indels 3; Gaps 1;  
QY 1 GPKGDDGKGDPEEGKHGKVGKGMGPKGKIGKGE--LQDMGDRNIGKTGPIGKKGDKGK 57  
DB 406 GPKGANGEPKAGEKGLPGAPGTGPKGAGPAGIAGPKGDRGVDGKPEGAPGDVGK 465  
QY 58 GLGIPGKKGKAG 70  
DB 466 GEVGPSPGQPGAKG 478

RESULT 14  
US-09-134-000C-6019  
Sequence 6019, Application US/09134000C  
Patent No. 6617156  
GENERAL INFORMATION:  
APPLICANT: Lynn Doucette-Stamm et al  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 032796-032  
CURRENT APPLICATION NUMBER: US/09/134,000C  
CURRENT FILING DATE: 1998-08-13  
PRIOR APPLICATION NUMBER: US 60/055,778  
PRIOR FILING DATE: 1997-08-15  
NUMBER OF SEQ ID NOS: 6812  
SOFTWARE: Patent in version 3.1  
SEQ ID NO 6019  
LENGTH: 399  
TYPE: PRT  
ORGANISM: Enterococcus faecalis  
US-09-134-000C-6019

Query Match 44.7%; Score 176; DB 4; Length 399;  
Best Local Similarity 49.3%; Pred. No. 2.9e-13;  
Matches 33; Conservative 11; Mismatches 23; Indels 0; Gaps 0;  
QY 1 GPKGDDGKGDPEEGKHGKVGKGMGPKGKIGKLGMDGRNIGKTGPIGKKGDKGKGLL 60  
DB 81 GPQGPSPKSGEAGLQGLTGAPKQKATGAPGPRGKSGKDGILGTGPKGHEGTKGDKGDL 140  
QY 61 GIPGKKGKAG 67  
DB 141 GPQGPSPGK 147

RESULT 15  
US-09-227-357-190  
; Sequence 190, Application US/09227357  
; Patent No. 6342581  
; GENERAL INFORMATION:  
; APPLICANT: Fischer et al.  
; TITLE OF INVENTION: 123 Human Secreted Proteins  
; FILE REFERENCE: P2010P1  
; CURRENT APPLICATION NUMBER: US/09/227,357  
; CURRENT FILING DATE: 1999-01-08  
; EARLIER APPLICATION NUMBER: PCT/US98/13684  
; EARLIER FILING DATE: 1998-07-07  
; EARLIER APPLICATION NUMBER: 60/051,926  
; EARLIER FILING DATE: 1997-07-08  
; EARLIER APPLICATION NUMBER: 60/052,793  
; EARLIER FILING DATE: 1997-07-08  
; EARLIER APPLICATION NUMBER: 60/051,925  
; EARLIER FILING DATE: 1997-07-08  
; EARLIER APPLICATION NUMBER: 60/051,929  
; EARLIER FILING DATE: 1997-07-08  
; EARLIER APPLICATION NUMBER: 60/052,803  
; EARLIER FILING DATE: 1997-07-08  
; EARLIER APPLICATION NUMBER: 60/052,732  
; EARLIER FILING DATE: 1997-07-08  
; EARLIER APPLICATION NUMBER: 60/051,931  
; EARLIER FILING DATE: 1997-07-08  
; EARLIER APPLICATION NUMBER: 60/051,932  
; EARLIER FILING DATE: 1997-07-08  
; EARLIER APPLICATION NUMBER: 60/051,916  
; EARLIER FILING DATE: 1997-07-08  
; EARLIER APPLICATION NUMBER: 60/051,930  
; EARLIER FILING DATE: 1997-07-08  
; EARLIER APPLICATION NUMBER: 60/051,918  
; EARLIER FILING DATE: 1997-07-08  
; EARLIER APPLICATION NUMBER: 60/051,920  
; EARLIER FILING DATE: 1997-07-08  
; EARLIER APPLICATION NUMBER: 60/052,733  
; EARLIER FILING DATE: 1997-07-08  
; EARLIER APPLICATION NUMBER: 60/052,795  
; EARLIER FILING DATE: 1997-07-08  
; EARLIER APPLICATION NUMBER: 60/051,919  
; EARLIER FILING DATE: 1997-07-08  
; EARLIER APPLICATION NUMBER: 60/051,928  
; EARLIER FILING DATE: 1997-07-08  
; EARLIER APPLICATION NUMBER: 60/055,722  
; EARLIER FILING DATE: 1997-08-18  
; EARLIER APPLICATION NUMBER: 60/055,723  
; EARLIER FILING DATE: 1997-08-18  
; EARLIER APPLICATION NUMBER: 60/055,948  
; EARLIER FILING DATE: 1997-08-18  
; EARLIER APPLICATION NUMBER: 60/055,949  
; EARLIER FILING DATE: 1997-08-18  
; EARLIER APPLICATION NUMBER: 60/055,953  
; EARLIER FILING DATE: 1997-08-18  
; EARLIER APPLICATION NUMBER: 60/055,950  
; EARLIER FILING DATE: 1997-08-18  
; EARLIER APPLICATION NUMBER: 60/055,947  
; EARLIER FILING DATE: 1997-08-18  
; EARLIER APPLICATION NUMBER: 60/055,964  
; EARLIER FILING DATE: 1997-08-18  
; EARLIER APPLICATION NUMBER: 60/056,360  
; EARLIER FILING DATE: 1997-08-18  
; EARLIER APPLICATION NUMBER: 60/055,684  
; EARLIER FILING DATE: 1997-08-18  
; EARLIER APPLICATION NUMBER: 60/055,984  
; EARLIER FILING DATE: 1997-08-18  
; EARLIER APPLICATION NUMBER: 60/055,954  
; EARLIER FILING DATE: 1997-08-18  
; EARLIER APPLICATION NUMBER: 60/058,785  
; EARLIER FILING DATE: 1997-09-12  
; EARLIER APPLICATION NUMBER: 60/058,664  
; EARLIER FILING DATE: 1997-09-12

; EARLIER APPLICATION NUMBER: 60/058,660  
; EARLIER FILING DATE: 1997-09-12  
; EARLIER APPLICATION NUMBER: 60/058,661  
; EARLIER FILING DATE: 1997-09-12  
; NUMBER OF SEQ ID NOS: 672  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 190  
; LENGTH: 128  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (127)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (128)  
; OTHER INFORMATION: Xaa equals stop translation  
US-09-227-357-190  
  
Query Match 44.3%; Score 174.5; DB 4; Length 128;  
Best Local Similarity 52.2%; Pred. No. 1.2e-13;  
Matches 35; Conservative 8; Mismatches 21; Indels 3; Gaps 1;  
  
QY 1 GPKGDDGKGDPPGEGKHGKVGKMGPKGKGGELGMDRGNIGKTPIGKKGDKGKGLL 60  
DB 62 GRDGRDGRGKGEKGTAGLRGKTGPLGLAGE---KGDQGETGKGPIGPEGEKGEVGP 118  
QY 61 GIPGEGK 67  
DB 119 GPPGPKG 125  
  
Search completed: March 8, 2004, 12:17:27  
Job time : 19.7137 secs

No good data

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 8, 2004, 11:54:00 ; Search time 66.2907 Seconds

(without alignments)  
306.882 Million cell updates/sec

Title: US-09-600-932-2\_COPY\_47\_118

Perfect score: 394

Sequence: 1 GPKGDDGKGPGEKGKHK.....DKGKGLLIPGKGRAGTV 72

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: Genesep29Jan04.\*
- 2: Genesep1980s.\*
- 3: Genesep1990s.\*
- 4: Genesep2000s.\*
- 5: Genesep2001s.\*
- 6: Genesep2002s.\*
- 7: Genesep2003as.\*
- 8: Genesep2003bs.\*
- 9: Genesep2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	394	100.0	277	2	AAV25518 Human col
2	390	99.0	277	2	AAV41698 Human PRO
3	390	99.0	277	3	AB44254 Human PRO
4	390	99.0	277	4	AAU29073 Human PRO
5	390	99.0	277	6	ABU58449 Human PRO
6	390	99.0	277	6	ABU87997 Novel hum
7	390	99.0	277	6	ABU84312 Human sec
8	390	99.0	277	6	ABR66186 Human sec
9	390	99.0	277	6	ABR65576 Human sec
10	390	99.0	277	6	ABU99516 Human sec
11	390	99.0	277	6	ABU82755 Human PRO
12	390	99.0	277	6	ABU8876 Novel hum
13	390	99.0	277	6	ABR68125 Human sec
14	390	99.0	277	6	ABU96178 Novel hum
15	390	99.0	277	6	ABU92609 Human sec
16	390	99.0	277	6	ABO08686 Human sec
17	390	99.0	277	6	ABO02738 Human sec
18	390	99.0	277	6	ABR74892 Human sec
19	390	99.0	277	6	ABR94654 Human sec
20	390	99.0	277	6	ABO25209 Novel hum
21	390	99.0	277	6	ABU85627 Human PRO
22	390	99.0	277	6	ABU98787 Novel hum
23	390	99.0	277	6	ABU98002 Novel hum
24	390	99.0	277	6	ABU91708 Novel hum
25	390	99.0	277	6	ABU72206 Novel hum

26	390	99.0	277	6	ABU89401 Human PRO
27	390	99.0	277	6	ABU86242 Human sec
28	390	99.0	277	6	ABU67455 Human sec
29	390	99.0	277	6	ABU80483 Human PRO
30	390	99.0	277	6	ABR99401 Human sec
31	390	99.0	277	6	ABR98791 Human sec
32	390	99.0	277	6	ABO16314 Human sec
33	390	99.0	277	6	ABR92214 Human sec
34	390	99.0	277	6	ABO18855 Human sec
35	390	99.0	277	6	ABR78276 Human sec
36	390	99.0	277	6	ABU85012 Novel hum
37	390	99.0	277	6	ABO00151 Human sec
38	390	99.0	277	6	ABO11483 Human sec
39	390	99.0	277	6	ABO02128 Human sec
40	390	99.0	277	6	ABU88702 Novel hum
41	390	99.0	277	6	ABU83397 Human sec
42	390	99.0	277	6	ABO06198 Novel hum
43	390	99.0	277	6	ABR59234 Human sec
44	390	99.0	277	6	ABO09296 Human sec
45	390	99.0	277	6	ABO19160 Novel hum

ALIGNMENTS

RESULT 1

AAV25518  
ID AAV25518 standard; protein; 277 AA.

XX AC AAV25518;

XX DT 30-SEP-1999 (first entry)

XX DE Human collectin protein.

XX KW Collectin; human; antibacterial; antiviral; treatment; infection.

XX OS Homo sapiens.

XX FN WO9937767-A1.

XX PD 29-JUL-1999.

XX PF 24-JUL-1998; 98WO-JP003328.

XX PR 23-JAN-1998; 98JP-00011281.

XX PA (FUSO ) FUSO PHARM IND LTD.

XX PI Wakamiya N;

XX DR WPI; 1999-458691/38.

XX DR N-PSDB; AAX88323.

XX PT New collectin protein of human origin and DNA encoding it.

XX PS Claim 1; Page 42-44; 58pp; Japanese.

XX CC This invention describes the isolation and characterisation of a novel human collectin protein and its encoding polynucleotide. The human collectin exhibits antibacterial and antiviral activity and can be used as an agent for the treatment of human bacterial and viral infections.

XX CC This sequence represents the novel human collectin

XX SQ Sequence 277 AA;

Query Match 100.0%; Score 394; DB 2; Length 277;

Best Local Similarity 100.0%; Pred. No. 8e-37;

Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPKGDDGKGPGEKGKHKVGRMGPKIKGELGDMGDRGNIGTKTGPICKGDKGKGLL 60

DB 47 GPKGDDGKGPGEKGKHKVGRMGPKIKGELGDMGDRGNIGTKTGPICKGDKGKGLL 106

QY	61	GIPGEKKGAGTV 72	27-APR-1998;	98US-00833336P.
Db	107	GIPGEKKGAGTV 118	28-APR-1998;	98US-00833322P.
			29-APR-1998;	98US-00833392P.
			29-APR-1998;	98US-00834395P.
			29-APR-1998;	98US-00834366P.
			29-APR-1998;	98US-00834393P.
			29-APR-1998;	98US-00835000P.
			29-APR-1998;	98US-00835545P.
			29-APR-1998;	98US-00835588P.
			29-APR-1998;	98US-00835599P.
			30-APR-1998;	98US-00837422P.
			05-MAY-1998;	98US-00843666P.
			06-MAY-1998;	98US-00844144P.
			06-MAY-1998;	98US-00844411P.
			07-MAY-1998;	98US-00845988P.
			07-MAY-1998;	98US-00846000P.
			07-MAY-1998;	98US-00846377P.
			07-MAY-1998;	98US-00846377P.
			07-MAY-1998;	98US-00846399P.
			07-MAY-1998;	98US-00846400P.
			07-MAY-1998;	98US-00846433P.
			13-MAY-1998;	98US-00853232P.
			13-MAY-1998;	98US-00853338P.
			13-MAY-1998;	98US-00853399P.
			15-MAY-1998;	98US-00855737P.
			15-MAY-1998;	98US-00855799P.
			15-MAY-1998;	98US-00855800P.
			15-MAY-1998;	98US-00855822P.
			15-MAY-1998;	98US-00856899P.
			15-MAY-1998;	98US-00856977P.
			15-MAY-1998;	98US-00857000P.
			15-MAY-1998;	98US-00857044P.
			18-MAY-1998;	98US-00860233P.
			22-MAY-1998;	98US-00863322P.
			22-MAY-1998;	98US-00864144P.
			22-MAY-1998;	98US-00864300P.
			22-MAY-1998;	98US-00864866P.
			28-MAY-1998;	98US-00870988P.
			28-MAY-1998;	98US-00871066P.
			28-MAY-1998;	98US-00872088P.
			30-JUL-1998;	98US-00946511P.
			11-SEP-1998;	98US-01000388P.
			(GETH ) GENENTECH INC.	
			Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;	
			WPI, 1999-551358/46.	
			N-PSDB; AA33973.	
			New secreted and transmembrane polypeptides and their polynucleotides, useful for treating blood coagulation disorders, cancers and cellular adhesion disorders.	
			Claim 12; Fig 37; 530pp; English.	
			The present invention describes secreted and transmembrane polypeptides and their polynucleotides. The nucleotide sequences are useful as sources of probes, primers, for chromosome mapping, and for generation of antisense sequences. They can also be used to create transgenic animals. The proteins can be used to treat a variety of diseases and disorders, depending on their function. Diseases that may be treated include blood coagulation disorders, cancers and cellular adhesion disorders. They may also be used to raise antibodies. AA33891 to AA34338, and AA41685 to AA41774 represent polynucleotide and polypeptide sequence given in the exemplification of the present invention	
			Sequence 277 AA;	
			Query Match	99.0%; Score 390; DB 2; Length 277;
			Best Local Similarity	98.6%; Pred. No. 2.3e-36;
			Matches	71; Conservative 1; Mismatches 0; Indels 0; Caps 0;

RESULT 2  
 ID AAY41698  
 AC AAY41698 standard; protein; 277 AA.  
 AC AAY41698;  
 XX 07-DEC-1999 (first entry)  
 DE Human PRO702 protein sequence.  
 KW Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;  
 KW probe; blood coagulation disorder; cancer; cellular adhesion disorder;  
 KW secreted protein; transmembrane protein.  
 OS Homo sapiens.  
 XX WO9946281-A2.  
 PD 16-SEP-1999.  
 XX 08-MAR-1999; 99WO-US005028.  
 XX 10-MAR-1998; 98US-0077450P.  
 PR 11-MAR-1998; 98US-0077632P.  
 PR 11-MAR-1998; 98US-0077641P.  
 PR 11-MAR-1998; 98US-0077649P.  
 PR 13-MAR-1998; 98US-0077791P.  
 PR 13-MAR-1998; 98US-0078004P.  
 PR 17-MAR-1998; 98US-00040220.  
 PR 20-MAR-1998; 98US-0078686P.  
 PR 20-MAR-1998; 98US-0078910P.  
 PR 20-MAR-1998; 98US-0078936P.  
 PR 20-MAR-1998; 98US-0078939P.  
 PR 25-MAR-1998; 98US-0079294P.  
 PR 26-MAR-1998; 98US-0079656P.  
 PR 27-MAR-1998; 98US-0079663P.  
 PR 27-MAR-1998; 98US-0079664P.  
 PR 27-MAR-1998; 98US-0079689P.  
 PR 27-MAR-1998; 98US-0079728P.  
 PR 27-MAR-1998; 98US-0079786P.  
 PR 30-MAR-1998; 98US-0079920P.  
 PR 30-MAR-1998; 98US-0079923P.  
 PR 31-MAR-1998; 98US-0080105P.  
 PR 31-MAR-1998; 98US-0080107P.  
 PR 31-MAR-1998; 98US-0080165P.  
 PR 01-APR-1998; 98US-0080194P.  
 PR 01-APR-1998; 98US-0080327P.  
 PR 01-APR-1998; 98US-0080328P.  
 PR 01-APR-1998; 98US-0080333P.  
 PR 01-APR-1998; 98US-0080334P.  
 PR 08-APR-1998; 98US-0081049P.  
 PR 08-APR-1998; 98US-0081070P.  
 PR 08-APR-1998; 98US-0081071P.  
 PR 09-APR-1998; 98US-0081195P.  
 PR 09-APR-1998; 98US-0081203P.  
 PR 09-APR-1998; 98US-0081229P.  
 PR 15-APR-1998; 98US-0081817P.  
 PR 15-APR-1998; 98US-0081838P.  
 PR 15-APR-1998; 98US-0081952P.  
 PR 15-APR-1998; 98US-0081955P.  
 PR 21-APR-1998; 98US-0082568P.  
 PR 21-APR-1998; 98US-0082569P.  
 PR 22-APR-1998; 98US-0082700P.  
 PR 22-APR-1998; 98US-0082704P.  
 PR 22-APR-1998; 98US-0082804P.  
 PR 23-APR-1998; 98US-0082767P.  
 PR 23-APR-1998; 98US-0082796P.

QY 1 GPKGDDGKGDGPEEGKHGKVGKGMGPKGKIGKGLGDMGDRNIGKTGPIGKKGDKGKGLL 60  
DB 47 GPKGDDGKGDGPEEGKHGKVGKGMGPKGKIGKGLGDMGDRNIGKTGPIGKKGDKGKGLL 106  
QY 61 GIPGKKGKAGTV 72  
DB 107 GIPGKKGKAGTV 118

RESULT 3  
AAB44254  
ID AAB44254 standard; protein; 277 AA.  
XX AAB44254;  
XX 08-FEB-2001 (first entry)  
XX Human PRO702 (UNQ366) protein sequence SEQ ID NO:97.  
DE Human; secreted protein; transmembrane protein; PRO; EST; cytosstatic;  
KW expressed sequence tag; detection; cancer.  
XX Homo sapiens.  
OS  
PN WO200053756-A2.  
XX  
XX 14-SEP-2000.  
XX  
XX 18-FEB-2000; 2000WO-US004341.  
XX  
XX 08-MAR-1999; 99WO-US005028.  
XX 13-MAR-1999; 99US-0123957P.  
XX 23-MAR-1999; 99US-0126773P.  
XX 21-APR-1999; 99US-0130232P.  
XX 28-APR-1999; 99US-0133445P.  
XX 14-MAY-1999; 99US-0134287P.  
XX 23-JUN-1999; 99US-0141037P.  
XX 26-JUL-1999; 99US-0145698P.  
XX 29-OCT-1999; 99US-0162506P.  
XX 30-NOV-1999; 99WO-US028313.  
XX 02-DEC-1999; 99WO-US028551.  
XX 02-DEC-1999; 99WO-US028565.  
XX 16-DEC-1999; 99WO-US030095.  
XX 30-DEC-1999; 99WO-US031243.  
XX 05-JAN-2000; 2000WO-US000219.  
XX 06-JAN-2000; 2000WO-US000272.  
XX 06-JAN-2000; 2000WO-US000376.  
XX  
XX (GETH ) GENENTECH INC.  
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen MB;  
PI Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;  
PI Kljavin LJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;  
PI Stewart TA, Tumas D, Williams PW, Wood WJ;  
XX WPI; 2000-611443/58.  
DR N-PSDB; AAC78480.  
XX  
XX Novel PRO polypeptides and polynucleotides used in detection methods, to  
PT target bioactive molecules to specific cells, and to modulate cellular  
PT activities.  
XX  
XX Claim 12; Fig 37; 636pp; English.  
XX  
XX AAC78458 to AAC78599 represent polynucleotide and EST (expressed sequence  
CC tag) sequences which encode secreted or transmembrane PRO polypeptides.  
CC The PRO polynucleotides and polypeptides have cytosstatic activity. The  
CC polynucleotides and polypeptides can be used for detecting the presence  
CC of PRO polypeptides in samples, for linking bioactive molecules to cells  
CC and for modulating biological activities of cells, using the polypeptides

CC for specific targeting. The polypeptide targeting can be used to kill the  
CC target cells, e.g. for the treatment of cancers. The polypeptide pairs  
CC provide specific targeting of bioactive molecules to cells. AAC78600 to  
CC AAC78987 represent PCR primers and probes used in the isolation of the  
CC PRO polynucleotide sequences  
XX  
SQ Sequence 277 AA;

Query Match 99.0%; Score 390; DB 3; Length 277;  
Best Local Similarity 98.6%; Pred. No. 2.3e-36;  
Matches 71; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GPKGDDGKGDGPEEGKHGKVGKGMGPKGKIGKGLGDMGDRNIGKTGPIGKKGDKGKGLL 60  
DB 47 GPKGDDGKGDGPEEGKHGKVGKGMGPKGKIGKGLGDMGDRNIGKTGPIGKKGDKGKGLL 106  
QY 61 GIPGKKGKAGTV 72  
DB 107 GIPGKKGKAGTV 118

RESULT 4  
AAU29073  
ID AAU29073 standard; protein; 277 AA.  
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XX  
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KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;  
KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;  
KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.  
XX  
XX Homo sapiens.  
XX  
XX WO200168848-A2.  
XX  
XX 20-SEP-2001.  
XX  
XX 28-FEB-2001; 2001WO-US006520.  
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XX 02-MAR-2000; 2000WO-US005841.  
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XX 15-MAR-2000; 2000WO-US006884.  
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XX 30-MAR-2000; 2000WO-US008439.  
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XX 17-MAY-2000; 2000WO-US013705.

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PR 05-JUN-2000; 2000US-0209832P.  
PR 28-JUL-2000; 2000WO-US020710.  
PR 22-AUG-2000; 2000US-00644848.  
PR 24-AUG-2000; 2000WO-US023328.  
PR 08-NOV-2000; 2000WO-US030952.  
PR 01-DEC-2000; 2000WO-US032678.  
PR 20-DEC-2000; 2000WO-US034956.  
XX (GETH ) GENENTECH INC.  
XX Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;  
PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;  
XX WPI; 2001-602746/68.  
DR N-PSDB; AAS45974.  
XX Novel nucleic acids encoding PRO polypeptides, used to diagnose the  
PT presence of tumors, such as prostate and breast tumors, in mammals and to  
PT screen for modulators of the compounds.  
XX Claim 11; Fig 100; 774pp; English.  
XX Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.  
CC The PRO polypeptides and their associated nucleic acids can be used to  
CC detect the presence of a tumour in a mammal by comparing the level of  
CC expression of a PRO polypeptide in a test sample of cells from the animal  
CC and a control sample of normal cells, whereby a higher level of  
CC expression in the test sample indicates the presence of a tumour in the  
CC mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats  
CC and rabbits but are preferably human. The polypeptides can be used to  
CC stimulate tumour necrosis factor (TNF) alpha release from human blood,  
CC when contacted with it. A specific polypeptide can be used to stimulate  
CC the proliferation or differentiation of chondrocyte cells. The PRO  
CC proteins can be used to determine the presence of tumours and also  
CC susceptibility to tumour development, particularly adrenal, lung, colon,  
CC breast, prostate, rectal, cervical, or liver tumours, in mammalian  
CC subjects. The oligonucleotide probes specific for the PRO nucleic acids  
CC can be used for genetic analysis of individuals with genetic disorders  
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Best Local Similarity 98.6%; Pred. No. 2.3e-36;  
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Db 107 GIFGEXGKAGTV 118  
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XX DT 15-APR-2003 (first entry)  
XX DE Human PRO polypeptide #50.  
XX KW Human; PRO; cystostatic; tumour; cancer; breast; lung; stomach; liver;  
KW dog; cat; cow; horse; sheep; pig; goat; rabbit; ADAPT;  
KW antibody-dependent enzyme mediated prodrug therapy.  
XX OS Homo sapiens.  
XX

PN US2003027272-A1.  
XX 06-FEB-2003.  
XX 21-JUN-2002; 2002US-00176492.  
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Db 107 GIPGKKGKAGTV 118

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ID ABU87997 standard; protein; 277 AA.  
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DT 07-JUL-2003 (first entry)  
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KW Human; secreted and transmembrane protein; PRO; gene therapy;  
KW tumour necrosis factor-alpha release; TNF-alpha release;  
KW chondrocyte proliferation; chondrocyte differentiation; tumour;  
KW adrenal tumour; lung tumour; colon tumour; breast tumour;  
KW prostate tumour; rectal tumour; cervical tumour; liver tumour.  
XX Homo sapiens.  
OS  
XX US2003032127-A1.



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XX KW tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;

XX KW tissue typing.

XX XX

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XX US2003032112-A1.

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KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;  
KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;  
KW liver; drug screening; transgenic animal; genetic analysis;  
KW antiarthritic; vulnery; gene therapy.  
XX  
OS Homo sapiens.  
XX  
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PD 06-FEB-2003.  
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XX KW Human; PRO polypeptide; secreted and transmembrane protein; tumour;
XX KW chromosome mapping; gene mapping; cytostatic.
XX OS Homo sapiens.
XX PN US2003032113-A1.
XX PD 13-FEB-2003.
XX PF 20-JUN-2002; 2002US-00176911.
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KW affinity purification.  
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KW extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
KW chondrocyte; proliferation; differentiation; cartilage disorder;
KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
KW liver; drug screening; transgenic animal; genetic analysis;
KW antiarthritic; vulnery; gene therapy.
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Db 107 GIPGKKGKAGTV 118  
  
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XX  
KW Human; secreted and transmembrane protein; PRO; transgenic animal;  
KW knockout; chromosome identification; tissue typing; tumour;  
KW chondrocyte proliferation; chondrocyte differentiation;  
tumor necrosis factor-alpha release stimulator.  
XX  
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Search completed: March 8, 2004, 12:11:22  
Job time : 66.2907 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 8, 2004, 11:56:05 ; Search time 4.5912 Seconds

(without alignments)  
328.331 Million cell updates/sec

Title: US-09-600-932-2\_COPY\_119\_147

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Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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27	44.5	29.1	164	1 YOH4 SALTI	Q82368 salmonella
28	44.5	29.1	164	1 YOH4 SALTY	Q82368 salmonella
29	44	28.8	126	1 YOH4 BACPA	P41021 bacillus pa
30	44	28.8	363	1 MRAY STROO	P56833 streptomyce
31	44	28.8	571	1 UREL STREP	O89595 staphylococ
32	44	28.8	975	1 KINH DROME	P17210 drosophila
33	44	28.8	1180	1 ITAI RAT	P18614 rattus norv

#### ALIGNMENTS

##### RESULT 1

ID	LMA5 MOUSE	STANDARD;	PRT;	3718 AA.
AC	O61001; 09JHO6;			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	15-MAR-2004 (Rel. 43, Last annotation update)			
DE	Laminin alpha-5 chain precursor.			
GN	LMA5.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.			
OX	NCBI_TaxID=10090;			
[1]				
RP	SEQUENCE OF 1-92 FROM N.A., AND SEQUENCE OF 41-46.			
RX	MEDLINE=21818471; PubMed=11829758;			
RA	Garbe J.H., Gohring W., Mann K., Timpl R., Sasaki T.;			
RT	"Complete sequence, recombinant analysis and binding to laminins and sulphated ligands of the N-terminal domains of laminin alpha3B and alpha5 chains.";			
RT	Biochem. J. 362:213-221 (2002).			
[2]				
RP	SEQUENCE OF 84-3718 FROM N.A.			
RC	STRAIN=C57BL/6 X CBA; TISSUE=Lung;			
RX	MEDLINE=96081906; PubMed=7499364;			
RA	Miner J.H., Lewis R.M., Sanes J.R.;			
RT	"Molecular cloning of a novel laminin chain, alpha 5, and widespread expression in adult mouse tissues.";			
RL	J. Biol. Chem. 270:28523-28526(1995).			
[3]				
RP	REVISIONS.			
RA	Miner J.H., Lewis R.M., Sanes J.R.;			
RL	Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.			
CC	-1- FUNCTION: Binding to cells via a high affinity receptor, laminin is thought to mediate the attachment, migration and organization of cells into tissues during embryonic development by interacting with other extracellular matrix components.			
CC	-1- FUNCTION: ALPHA-5 CHAIN MAY BE THE MAJOR LAMININ ALPHA CHAIN OF ADULT EPITHELIAL AND/OR ENDOTHELIAL BASAL LAMINAE.			
CC	-1- SUBUNIT: Laminin is a complex glycoprotein, consisting of three different polypeptide chains (alpha, beta, gamma), which are bound to each other by disulfide bonds into a cross-shaped molecule comprising one long and three short arms with globules at each end.			
CC	-1- SUBCELLULAR LOCATION: Extracellular; found in the basement membranes (major component).			
CC	-1- TISSUE SPECIFICITY: In adult, high levels in heart, lung, and kidney; lower in brain, muscle and testis; very low in liver, gut and skin.			
CC	-1- DOMAIN: The alpha-helical domains I and II are thought to interact with other laminin chains to form a coiled coil structure.			
CC	-1- DOMAIN: Domains VI, IV and G are globular.			
CC	-1- SIMILARITY: Contains 1 laminin N-terminal domain.			
CC	-1- SIMILARITY: Contains 22 laminin EGF-like domains.			
CC	-1- SIMILARITY: Contains 2 laminin IV domains.			
CC	-1- SIMILARITY: Contains 5 laminin G-like domains.			





```
Query Match          34.0%; Score 52; DB 1; Length 3718;
Best Local Similarity 43.5%; Pred. No. 17;
Matches 10; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 4 GRYKFKVQGLDISIARLKTSMK 26
DB 2719 GVRKLIQAARSAAKVKSMKF 2741

RESULT 2
PLE1_CRIGR STANDARD; PRT; 4473 AA.
AC Q9J155;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Plectin 1 (PLTN) (PCN) (300-kDa intermediate filament-associated
DE protein) (IFAP300) (Fragment).
GN PLECI.
OS Cricetus griseus (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Cricetulus.
OX NCBI_TaxID=10029;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20334248; PubMed=10873583;
RA Clubb B.H., Chou Y.-H., Herrmann H., Svitekina T.M., Borisy G.G.,
RA Goldman R.D.;
RT "The 300-kDa intermediate filament-associated protein (IFAP300) is a
RT hamster plectin ortholog.";
RL Biochem. Biophys. Res. Commun. 273:183-187(2000).
RN [2]
RP PHOSPHORYLATION.
RX MEDLINE=96215219; PubMed=8626512;
RA Malecz N., Foissner R., Stadler C., Wiche G.;
RT Identification of plectin as a substrate of p34cdc2 kinase and
RT mapping of a single phosphorylation site.";
RL J. Biol. Chem. 271:8203-8208(1996).
CC -!- FUNCTION: Interlinks intermediate filaments with microtubules and
CC microfilaments and anchors intermediate filaments to desmosomes or
CC hemidesmosomes. May be involved not only in the crosslinking and
CC stabilization of cytoskeletal intermediate filaments network, but
CC also in the regulation of their dynamics.
CC -!- SUBUNIT: Homodimer or homotetramer.
CC -!- DOMAIN: The N-terminus interacts with actin, the C-terminus with
CC vimentin, desmin, GFAP, cyokeratins, lamin B; whereas both the N-
CC and the C-terminus can bind integrin beta-4.
CC -!- PTM: PHOSPHORYLATED BY CDC2; REGULATES DISSOCIATION FROM
CC INTERMEDIATE FILAMENTS DURING MITOSIS.
CC -!- SIMILARITY: Contains 1 actin-binding domain.
CC -!- SIMILARITY: Contains 2 calponin-homology (CH) domains.
CC -!- SIMILARITY: Contains 32 plectin repeats.
CC -!- SIMILARITY: Contains 4 spectrin repeats.
CC -!- SIMILARITY: Belongs to the plakin or cytolinker family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC HMBL; AF260753; AAF70372.1; ..
CC DR HMBL; Q01082; 1BKX.
CC DR InterPro; IPR001589; Actbind actin.
CC DR InterPro; IPR001715; Calponin-like.
CC DR InterPro; IPR001101; Plectin_repeat.
CC DR InterPro; IPR002017; Spectrin.
CC DR Pfam; PF00307; CH; 2.
CC DR Pfam; PF00681; Plectin; 20.

DR SMART; SM00033; CH; 2.
DR SMART; SM00250; PLEC; 34.
DR PROSITE; PS00019; ACTININ_1; PARTIAL.
DR PROSITE; PS00020; ACTININ_2; FALSE_NEG.
DR PROSITE; PS00021; CH; 2.
KW Coiled coil; Repeat; Structural protein; Cytoskeleton; Actin-binding;
KW Phosphorylation.
FT NON_TER 1
FT DOMAIN 1 1259
FT FT DOMAIN 1.
FT FT DOMAIN 1260 2544
FT FT DOMAIN 2545 4473
FT FT DOMAIN 192
FT FT DOMAIN 1.
FT FT DOMAIN 74
FT FT DOMAIN 87
FT FT DOMAIN 189
FT FT REPEAT 449 508
FT FT REPEAT 529 613
FT FT REPEAT 626 719
FT FT REPEAT 1104 1204
FT FT DOMAIN 1258 2548
FT FT REPEAT 2615 2652
FT FT REPEAT 2653 2690
FT FT REPEAT 2691 2728
FT FT REPEAT 2729 2766
FT FT REPEAT 2770 2804
FT FT REPEAT 2905 2942
FT FT REPEAT 2943 2980
FT FT REPEAT 2981 3018
FT FT REPEAT 3019 3056
FT FT REPEAT 3057 3094
FT FT REPEAT 3274 3311
FT FT REPEAT 3312 3349
FT FT REPEAT 3350 3387
FT FT REPEAT 3388 3425
FT FT REPEAT 3429 3463
FT FT REPEAT 3609 3646
FT FT REPEAT 3647 3684
FT FT REPEAT 3685 3722
FT FT REPEAT 3723 3760
FT FT REPEAT 3764 3797
FT FT REPEAT 3800 3834
FT FT REPEAT 3852 3889
FT FT REPEAT 3890 3927
FT FT REPEAT 3928 3965
FT FT REPEAT 3966 4003
FT FT REPEAT 4007 4041
FT FT REPEAT 4043 4094
FT FT REPEAT 4197 4234
FT FT REPEAT 4235 4272
FT FT REPEAT 4273 4310
FT FT REPEAT 4311 4348
FT FT REPEAT 4349 4386
FT FT DOMAIN 4039 4089
FT FT DOMAIN 4414 4429
FT FT MOD_RES 4328 4328
FT FT SEQUENCE 4473 AA; 509015 MW; E144615D361E3484 CRC64;

Query Match          33.3%; Score 51; DB 1; Length 4473;
Best Local Similarity 45.5%; Pred. No. 29;
Matches 10; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 4 GRYKFKVQGLDISIARLKTSMK 25
DB 514 GAYRECLGRDLQYAKLLNSK 535

RESULT 3
FA10_BOVIN
ID FA10_BOVIN STANDARD; PRT; 492 AA.
AC P00743;
DT 21-JUL-1986 (Rel. 01, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
```

DE Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor).  
GN 210.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidae;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]\_SEQUENCE OF 1-487 FROM N.A.  
RP MEDLINE=84247315; PubMed=6330671;  
RA Fung M.R., Campbell R.M., McGillivray R.T.A.;  
RT "Blood coagulation factor X mRNA encodes a single polypeptide chain  
RT containing a prepro leader sequence."  
RL Nucleic Acids Res. 12:4481-4492(1984).  
RN [2]  
RP SEQUENCE OF 41-180.  
RX MEDLINE=80130563; PubMed=6766735;  
RA Enfield D.L., Ericsson L.H., Fujikawa K., Walsh K.A., Neurath H.,  
RA Titani K.;  
RT "Amino acid sequence of the light chain of bovine factor X1 (Stuart  
RT factor).";  
RL Biochemistry 19:659-667(1980).  
RN [3]  
RP REVISION TO 103.  
RX MEDLINE=83308813; PubMed=6688526;  
RA McMullen B.A., Fujikawa K., Kisiel W.;  
RT "The occurrence of beta-hydroxyaspartic acid in the vitamin  
RT K-dependent blood coagulation zymogens."  
RL Biochem. Biophys. Res. Commun. 115:8-14(1983).  
RN [4]  
RP SEQUENCE OF 183-492, CARBOHYDRATE-LINKAGE SITES, AND DISULFIDE BONDS.  
RX MEDLINE=76053069; PubMed=1059093;  
RA Titani K., Fujikawa K., Enfield D.L., Ericsson L.H., Walsh K.A.,  
RA Neurath H.;  
RT "Bovine factor X1 (Stuart factor): amino-acid sequence of heavy  
RT chain."  
RL Proc. Natl. Acad. Sci. U.S.A. 72:3082-3086(1975).  
RN [5]  
RP SEQUENCE OF 183-233, AND CARBOHYDRATE-LINKAGE SITES.  
RX MEDLINE=94062825; PubMed=8243461;  
RA Inoue K., Morita T.;  
RT "Identification of O-linked oligosaccharide chains in the activation  
RT peptides of blood coagulation factor X. The role of the carbohydrate  
RT moieties in the activation of factor X."  
RL Eur. J. Biochem. 218:153-163(1993).  
RN [6]  
RP ACTIVE SITE.  
RX MEDLINE=73053314; PubMed=4264286;  
RA Titani K., Hermodson M.A., Fujikawa K., Ericsson L.H., Walsh K.A.,  
RA Neurath H., Davie E.W.;  
RT "Bovine factor X1a (activated Stuart factor). Evidence of homology  
RT with mammalian serine proteases."  
RL Biochemistry 11:4899-4903(1972).  
RN [7]  
RP PROCESSING.  
RX MEDLINE=76053121; PubMed=1059122;  
RA Fujikawa K., Titani K., Davie E.W.;  
RT "Activation of bovine factor X (Stuart factor): conversion of factor  
RT Xa-alpha to factor Xa-beta."  
RL Proc. Natl. Acad. Sci. U.S.A. 72:3359-3363(1975).  
RN [8]  
RP CALCIUM-BINDING DATA.  
RX MEDLINE=84185716; PubMed=6546930;  
RA Sugo T., Bjoerk I., Holmgren A., Stenflo J.;  
RT "Calcium-binding properties of bovine factor X lacking the gamma-  
RT carboxyglutamic acid-containing region."  
RL J. Biol. Chem. 259:5705-5710(1984).  
RN [9]  
RP SULFATION.  
RX MEDLINE=86140210; PubMed=3949800;  
RA Morita T., Jackson C.M.;  
RT "Localization of the structural difference between bovine blood  
RT coagulation factors X1 and X2 to tyrosine 18 in the activation

peptide".  
J. Biol. Chem. 261:4008-4014(1986).  
RN [10]  
RP STRUCTURE BY NMR OF 85-126.  
RX MEDLINE=91084483; PubMed=2261466;  
RA Selander M., Persson E., Stenflo J., Drakenberg T.;  
RT "1H NMR assignment and secondary structure of the Ca2(+)-free form of  
RT the amino-terminal epidermal growth factor like domain in coagulation  
RT factor X";  
RL Biochemistry 29:8111-8118(1990).  
RN [11]  
RP STRUCTURE BY NMR OF 85-136.  
RX MEDLINE=92329412; PubMed=1627540;  
RA Ullner M., Selander M., Persson E., Stenflo J., Drakenberg T.,  
RA Telemann O.;  
RT "Three-dimensional structure of the apo form of the N-terminal  
RT EGF-like module of blood coagulation factor X as determined by NMR  
RT spectroscopy and simulated folding."  
RL Biochemistry 31:5974-5983(1992).  
RN [12]  
RP STRUCTURE BY NMR OF 85-126.  
RX MEDLINE=92406922; PubMed=1527084;  
RA Selander-Sunnerhagen M., Ullner M., Persson E., Telemann O.,  
RA Stenflo J., Drakenberg T.;  
RT "How an epidermal growth factor (EGF)-like domain binds calcium. High  
RT resolution NMR structure of the calcium form of the NH2-terminal EGF-  
RT like domain in coagulation factor X."  
RL J. Biol. Chem. 267:19642-19649(1992).  
RN [13]  
RP STRUCTURE BY NMR OF 41-126.  
RX MEDLINE=96387194; PubMed=8794734;  
RA Sunnerhagen M., Olah G.A., Stenflo J., Forsen S., Drakenberg T.,  
RA Tremella J.;  
RT "The relative orientation of Gla and EGF domains in coagulation  
RT factor X is altered by Ca2+ binding to the first EGF domain. A  
RT combined NMR-small angle X-ray scattering study."  
RL Biochemistry 35:11547-11559(1996).  
RN [14]  
RP FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that  
RP converts prothrombin to thrombin in the presence of factor Va,  
RP calcium and phospholipid during blood clotting.  
CC CARBOLACTIC ACTIVITY: Preferential cleavage: Arg-|-Thr and then  
CC Arg-|-Ile bonds in prothrombin to form thrombin.  
CC ARG-|-SUBUNIT: The two chains are formed from a single-chain precursor  
CC by the excision of two Arg residues and are held together by 1 or  
CC more disulfide bonds.  
CC FUNCTION: The vitamin K-dependent, enzymatic carboxylation of some  
CC glutamate residues allows the modified protein to bind calcium.  
CC FUNCTION: N- and O-glycosylated.  
CC FUNCTION: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE  
CC INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY).  
CC MISCELLANEOUS: Calcium also binds, with stronger affinity to  
CC another site, beyond the Gla domain.  
CC SIMILARITY: Belongs to peptidase family S1.  
CC SIMILARITY: Contains 2 EGF-like domains.  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation  
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CC  
CC EMBL; X00673; CAA25286.1; --  
CC PIR; A22867; EXBO.  
CC PDB; 1AFO; 31-JAN-94.  
CC PDB; 1CCF; 31-MAY-94.  
CC PDB; 1WHE; 15-MAY-97.  
CC PDB; 1WHP; 15-MAY-97.  
CC PDB; 1IOD; 21-JAN-03.  
CC PDB; 1KIG; 28-OCT-98.  
CC MEROPS; S01.216; --  
CC GlycoSuiteDB; P00743; --

```

DR InterPro: IPR000152; Asx hydroxyl S.
DR InterPro: IPR000903; Cys_ser_trypsin.
DR InterPro: IPR000742; EGF_2.
DR InterPro: IPR001881; EGF_Ga.
DR InterPro: IPR006209; EGF_like.
DR InterPro: IPR002383; GLA blood.
DR InterPro: IPR001254; Peptidase S1.
DR InterPro: IPR001314; Peptidase S1A.
DR InterPro: IPR000294; VitK_dep_GLA.
DR Pfam: PF00008; EGF; 2.
DR Pfam: PF00594; GlA; 1.
DR Pfam: PF00089; trypsin; 1.
DR PRINTS: PR00722; GLABLOOD.
DR PRINTS: PR00001; GLABLOOD.
DR SMART: SM00179; EGF_CA; 1.
DR SMART: SM00069; GLA; 1.
DR SMART: SM00020; Tryp_Spc; 1.
DR PROSITE: PS00010; ASX_HYDROXYL; 1.
DR PROSITE: PS00022; EGF_1; 1.
DR PROSITE: PS01186; EGF_2; 1.
DR PROSITE: PS01187; EGF_CA; 1.
DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE: PS00240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; 1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
DR Glycoprotein; Hydrolase; Serine protease; Plasma; Blood coagulation;
KW Gamma-carboxyglutamic acid; Hydroxylation; Calcium-binding; Vitamin K;
KW Signal; Zymogen; EGF-like domain; Repeat; Sulfation; 3D-structure.
FT SIGNAL 1 23
FT PROPEP 24 40
FT CHAIN 41 180
FT CHAIN 181 492
FT PROPEP 183 233
FT CHAIN 234 492
FT PROPEP 476 492
FT DOMAIN 86 122
FT DOMAIN 125 165
FT DOMAIN 234 492
FT ACT_SITE 275 321
FT ACT_SITE 321 418
FT ACT_SITE 418 477
FT MOD_RES 46 46
FT MOD_RES 47 47
FT MOD_RES 54 54
FT MOD_RES 56 56
FT MOD_RES 59 59
FT MOD_RES 60 60
Query Match 32.0%; Score 49; DB 1; Length 492;
Best Local Similarity 40.0%; Pred. No. 6.1;
Matches 10; Conservative 6; Mismatches 9; Indels 0; Gaps 0;
QY 5 RYRKFGVGLDLSIARKLTKSMKFKVN 29
DB 312 RFVKETYPDFDIAVLRLTKTFIRFRN 336
RESULT 4
ID PLE1_MOUSE STANDARD; PRT; 964 AA.
AC Q9QXS1; Q9CS65; Q9QUT2; Q9QXQ8; Q9QXQ9; Q9QXR0; Q9QXR1; Q9QXR2;
AC Q9QXR3; Q9QXR4; Q9QXR5; Q9QXR6; Q9QXR7; Q9QXR8; Q9QXR9; Q9QXS0;
AC Q9QXS2; Q9QXS3;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Plectin 1 (PLTN) (PCN) (fragment).
GN PLEC1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND TISSUE SPECIFICITY.
RC TISSUE=Brain, Embryo, Heart, Kidney, Skeletal muscle, and Testis;
RX MEDLINE=20025755; PubMed=10556294;
RA Fuchs P., Zoerer M., Reznicek G.A., Spazierer D., Oehler S.,
RA Castanon M.J., Hauptmann R., Wiche G.;
RT "Unusual 5' transcript complexity of plectin isoforms: novel tissue-
specific exons modulate actin binding activity.";
RL Hum. Mol. Genet. 8:2461-2472(1999).
RN [2]
RP SEQUENCE OF 181-812 FROM N.A.
RC STRAIN=CS7BL/6J; TISSUE=Embryo;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Kawakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojochori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombarts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
CC -!- FUNCTION: Interlinks intermediate filaments with microtubules and
microfilaments and anchors intermediate filaments to desmosomes or
hemidesmosomes. May be involved not only in the crosslinking and
stabilization of cytoskeletal intermediate filaments network, but
also in the regulation of their dynamics.
CC -!- SUBUNIT: Homodimer or homotetramer (By similarity).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=16;
CC Name=PLEC-1.2A;
CC IsoId=Q9QXS1-1; Sequence=VSP_005048;
CC Name=PLEC-1;
CC IsoId=Q9QXS1-2; Sequence=VSP_005048;
CC Name=PLEC-1A;
CC IsoId=Q9QXS1-3; Sequence=VSP_005036, VSP_005045, VSP_005048;
CC Name=PLEC-1B.2A;
CC IsoId=Q9QXS1-4; Sequence=VSP_005037, VSP_005045;
CC Name=PLEC-1B;
CC IsoId=Q9QXS1-5; Sequence=VSP_005037, VSP_005045, VSP_005048,
VSP_005048;
CC Name=PLEC-0.1C;
CC IsoId=Q9QXS1-6; Sequence=VSP_005039, VSP_005047, VSP_005048;
CC Name=PLEC-0.1C.2A;
CC IsoId=Q9QXS1-7; Sequence=VSP_005039;
CC Name=PLEC-0.1C.2A.3A;
CC IsoId=Q9QXS1-8; Sequence=VSP_005039, VSP_005047, VSP_005049;
CC Name=PLEC-1D.2A;
CC IsoId=Q9QXS1-9; Sequence=VSP_005032, VSP_005041;
CC Name=PLEC-1D;
CC IsoId=Q9QXS1-10; Sequence=VSP_005032, VSP_005041, VSP_005048;
CC Name=PLEC-1E.2A;
CC IsoId=Q9QXS1-11; Sequence=VSP_005033;
CC Name=PLEC-1E;
CC IsoId=Q9QXS1-12; Sequence=VSP_005033, VSP_005042, VSP_005048;
CC Name=PLEC-1F;
CC IsoId=Q9QXS1-13; Sequence=VSP_005034, VSP_005043, VSP_005048;
CC Name=PLEC-1G;
CC IsoId=Q9QXS1-14; Sequence=VSP_005038, VSP_005046, VSP_005048;
CC Name=PLEC-1H;
CC IsoId=Q9QXS1-15; Sequence=VSP_005040;

```

CC Name=PLEC-11;  
CC IsoId=Q9XSI-16; Sequence=VSP\_005035, VSP\_005044;  
CC TISSUE SPECIFICITY: Expressed at high levels in lung, brain, small  
CC intestine, muscle, heart and skin with lower levels found in  
CC kidney, liver, uterus, spleen and salivary gland.  
CC -1- DOMAIN: The N-terminus interacts with actin, the C-terminus with  
CC vimentin, desmin, GAP, cytochromes, lamin B; whereas both the N-  
CC and the C-terminus can bind integrin beta-4.  
CC -1- PTM: PHOSPHORYLATED BY CDC2; REGULATES DISSOCIATION FROM  
CC INTERMEDIATE FILAMENTS DURING MITOSIS (BY SIMILARITY?).  
CC -1- SIMILARITY: Contains 1 actin-binding domain.  
CC -1- SIMILARITY: Contains 2 calponin-homology (CH) domains.  
CC -1- SIMILARITY: Contains 3 spectrin repeats.  
CC -1- SIMILARITY: Belongs to the plakin or cytolinker family.  
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CC -----  
CC EMBL; AF188006; AAF18066.1; -;  
CC EMBL; AF188007; AAF18067.1; -;  
CC EMBL; AF188008; AAF18068.1; -;  
CC EMBL; AF188009; AAF18069.1; -;  
CC EMBL; AF188010; AAF18070.1; -;  
CC EMBL; AF188011; AAF18071.1; -;  
CC EMBL; AF188012; AAF18072.1; -;  
CC EMBL; AF188013; AAF18073.1; -;  
CC EMBL; AF188014; AAF18074.1; -;  
CC EMBL; AF188015; AAF18075.1; -;  
CC EMBL; AF188016; AAF18076.1; -;  
CC EMBL; AF188017; AAF18077.1; -;  
CC EMBL; AF188018; AAF18078.1; -;  
CC EMBL; AF188019; AAF18079.1; -;  
CC EMBL; AF188020; AAF18080.1; -;  
CC EMBL; AF188021; AAF18081.1; -;  
CC EMBL; AF188022; AAF18082.1; -;  
CC EMBL; AF188023; AAF18083.1; -;  
CC EMBL; AF188024; AAF18084.1; -;  
CC MGD; MGI:1277961; Plect1.  
CC InterPro; IPR001589; Actbind actinin.  
CC InterPro; IPR001715; Calponin-like.  
CC InterPro; IPR005346; S10\_plectin\_N.  
CC InterPro; IPR002017; Spectrin.  
CC Pfam; PF00307; CH; 2.  
CC Pfam; PF03501; S10\_plectin; 1.  
CC Pfam; PF00435; spectrin; 2.  
CC ProDom; PD006662; S10\_plectin\_N; 1.  
CC ProSite; PS00019; ACTININ\_1; 1.  
CC ProSite; PS00020; ACTININ\_2; FALSE\_NEG.  
CC ProSite; PS00021; CH; 2.  
CC Repeat; Structural protein; Cytoskeleton; Actin-binding;  
KW Alternative splicing.  
FT DOMAIN 1 >964 GLOBULAR.  
FT DOMAIN 181 411 ACTIN-BINDING.  
FT DOMAIN 185 293 CH 1.  
FT DOMAIN 305 408 CH 2.  
FT REPEAT 653 727 SPECTRIN 1.  
FT REPEAT 748 832 SPECTRIN 2.  
FT REPEAT 845 938 SPECTRIN 3.  
FT VARSPLIC 1 5 MWAGM -> MKTVP (in isoform PLEC-1D and  
FT isoform PLEC-1D,2A).  
FT VARSPLIC 1 15 MWAGMPLDLRLAI -> MDPSRAIQHEISSLK (in  
FT isoform PLEC-1E and isoform PLEC-1E,2A).  
FT VARSPLIC 1 28 MWAGMPLDLRLAIYEVLFREGVWVAK -> MAHLITSGP  
FT PFDQDFIQAYEVEKRYK (in isoform PLEC-1F).  
FT VARSPLIC 1 33 MWAGMPLDLRLAIYEVLFREGVWVAKDRRP -> MNET

FT VRRKLSPSGSTNTLSRLRGTSVTCTKTS (in isoform  
FT PLEC-1I).  
FT /FTid=VSP\_005035.  
FT MWAGMPLDLRLAIYEVLFREGVWVAKDRRPRLH ->  
FT MSQRHLRVPEPEGSGKRTSSDNLVLAVLASEGKK (in  
FT isoform PLEC-1A).  
FT /FTid=VSP\_005036.  
FT MWAGMPLDLRLAIYEVLFREGVWVAKDRRPRLH ->  
FT MEPSGSLFPLSLVVGHVVTIAAVHWKKGHROAKDEQ (in  
FT isoform PLEC-1B and isoform PLEC-1B,2A).  
FT /FTid=VSP\_005037.  
FT MWAGMPLDLRLAIYEVLFREGVWVAKDRRPRLHHPV  
FT GVT -> MAGTWAARGVTSQREVLLEPCWLDGCEQVRR  
FT GYLGLQCCV (in isoform PLEC-1G).  
FT /FTid=VSP\_005038.  
FT MWAGMPLDLRLAIYEVLFREGVWVAKDRRPRLHHPV  
FT GVTNLQVWRAWSLKARG-VRETF -> MSGEDSEVRVA  
FT VARGSSNGSGSPGDTLPWLKGTORRRSGSGVNGS  
FT VLDPAERAVIRIA (in isoform PLEC-0,1C,  
FT isoform PLEC-0,1C,2A,3A and isoform  
FT PLEC-0,1C,2A).  
FT /FTid=VSP\_005039.  
FT Missing (in isoform PLEC-1H).  
FT /FTid=VSP\_005040.  
FT Missing (in isoform PLEC-1D and isoform  
FT PLEC-1D,2A).  
FT /FTid=VSP\_005041.  
FT Missing (in isoform PLEC-1B).  
FT /FTid=VSP\_005042.  
FT Missing (in isoform PLEC-1F).  
FT /FTid=VSP\_005043.  
FT Missing (in isoform PLEC-1I).  
FT /FTid=VSP\_005044.  
FT Missing (in isoform PLEC-1A, isoform  
FT PLEC-1B and isoform PLEC-1B,2A).  
FT /FTid=VSP\_005045.  
FT Missing (in isoform PLEC-1G).  
FT /FTid=VSP\_005046.  
FT Missing (in isoform PLEC-0,1C and isoform  
FT PLEC-0,1C,2A,3A).  
FT /FTid=VSP\_005047.  
FT Missing (in isoform PLEC-1, isoform  
FT VARSPLIC 202  
Query Match 32.0%; Score 49; DB 1; Length 964;  
Best Local Similarity 45.5%; Pred. No. 12;  
Matches 10; Conservative 4; Mismatches 8; Indels 0; Gaps 0;  
QY 4 GRYKFKVQLDISIARLKTSMK 25  
DB 733 GAYRDCLGRDLQYAKLNSK 754  
RESULT 5  
TOP2\_CRIFA  
ID TOP2\_CRIFA STANDARD; PRT; 1239 AA.  
DT 01-AUG-1992 (Rel. 23, Created)  
DT 01-AUG-1992 (Rel. 23, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE DNA topoisomerase II (EC 5.99.1.3).  
GN TOP2  
OS Crithidia fasciculata.  
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Crithidia.  
OX NCBI\_TaxID=5656;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CFCl;  
RA MEDLINE=9211798; PubMed=1311798;  
RA Pasion S.G., Hines J.C., Rebersold R., Ray D.S.;  
RT "Molecular cloning and expression of the gene encoding the  
RT kinetoplast-associated type II DNA topoisomerase of Crithidia  
RT fasciculata."  
RL Mol. Biochem. Parasitol. 50:57-68(1992).





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Proc. Natl. Acad. Sci. U.S.A. 93:4278-4283(1996).
[3]
RN PARTIAL SEQUENCE FROM N.A. (ISOFORMS 2; 3 AND 4), AND TISSUE
RP SPECIFICITY.
RC TISSUE=Glial tumor;
RX MEDLINE=97321050; PubMed=9177781;
RA Elliott C.E., Becker B., Oehler S., Castanon M.J., Hauptmann R.,
RA Wiche G.;
RT "Plectin transcript diversity: identification and tissue distribution
RT of variants with distinct first coding exons and rodless isoforms.";
RL Genomics 42:115-125(1997).
CC
CC !- FUNCTION: Interlinks intermediate filaments with microtubules and
CC microfilaments and anchors intermediate filaments to desmosomes or
CC hemidesmosomes. May be involved not only in the crosslinking and
CC stabilization of cytoskeletal intermediate filaments network, but
CC also in the regulation of their dynamics.
CC !- SUBUNIT: Homodimer or homotetramer.
CC !- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=4;
CC Name=1;
CC IsoId=P30427-1; Sequence=Displayed;
CC Name=2;
CC IsoId=P30427-2; Sequence=VSP_005050;
CC Name=3;
CC IsoId=P30427-3; Sequence=VSP_005051;
CC Name=4;
CC IsoId=P30427-4; Sequence=VSP_005052;
CC !- TISSUE SPECIFICITY: Widely expressed with highest expression in
CC skeletal muscle and lowest in thymus.
CC !- DOMAIN: The N-terminus interacts with actin, the C-terminus with
CC vimentin, desmin, GFAP, cytokeratins, lamin B; whereas both the N-
CC and the C-terminus can bind integrin beta-4.
CC !- PTM: PHOSPHORYLATED BY CDC2; REGULATES DISSOCIATION FROM
CC INTERMEDIATE FILAMENTS DURING MITOSIS (BY SIMILARITY).
CC !- SIMILARITY: Contains 1 actin-binding domain.
CC !- SIMILARITY: Contains 2 calponin-homology (CH) domains.
CC !- SIMILARITY: Contains 33 plectin repeats.
CC !- SIMILARITY: Contains 4 spectrin repeats.
CC !- SIMILARITY: Belongs to the plakin or cytolinker family.
CC !- CAUTION: Isoform 4 is a fragment at the N-terminus.
CC
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CC
CC EMBL; X59601; CAA42169.1; -
CC EMBL; U96274; AAC53209.1; -
CC EMBL; U96275; AAC53210.1; -
CC EMBL; U96276; AAC53211.1; -
CC FIC; A39638; A39638.
CC HSRP; Q01082; 1BRX.
CC
CC InterPro; IPR001589; Actbind_actnin.
CC InterPro; IPR001715; Calponin-like.
CC InterPro; IPR001101; Plectin repeat.
CC InterPro; IPR005326; S10_plectin_N.
CC InterPro; IPR002017; Spectrin.
CC Pfam; PF00307; CH; 2.
CC Pfam; PF00681; Plectin; 21.
CC Pfam; PF03501; S10_plectin; 1.
CC ProDom; PD006662; S10_plectin_N; 1.
CC SMART; SM00033; CH; 2.
CC SMART; SM00250; PLEC; 33.
CC SMART; SM00150; SPEC; 6.
CC
CC PROSITE; PS00019; ACTININ_1; FALSE_NEG.
CC PROSITE; PS00020; ACTININ_2; FALSE_NEG.
CC PROSITE; PS0021; CH; 2.
CC Coiled coil; Repeat; Structural protein; Cytoskeleton; Actin-binding;
CC Phosphorylation; Alternative splicing.
CC DOMAIN 1 1473
CC FT GLOBULAR.1

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RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,  
RA Woodward J., Volckaert G., Aert R., Robben J., Grymoprez B.,  
RA Weltjens I., Vansreels E., Rieger M., Schaefer M., Mueller-Auer S.,  
RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,  
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,  
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,  
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,  
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,  
RA Lucas M., Rochet M., Gallardin C., Tallada V.A., Garzon A., Thode G.,  
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,  
RA Carrutierrez A., Revuelta J.L., Moreno S., Armstrong J., Forsberg S.L.,  
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,  
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.,  
RT "The genome sequence of Schizosaccharomyces pombe."  
RL Nature 415:871-880(2002).  
CC -!- SIMILARITY: Belongs to the CBP3 family.  
CC  
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CC  
CC EMBL; AL132870; CAB60691.1; -  
CC PIR; T50431; T50431.  
CC GeneDB SPombe; SPOC4B3.17; -  
CC InterPro; IPR007129; Ubiquitin C chap.  
CC Pfam; PF03981; Ubiquitin C chap; 1.  
CC SEQUENCE 283 AA; 32972 MW; E32523E420029579 CRC64;  
SQ  
Query Match 30.7%; Score 47; DB 1; Length 283;  
Best Local Similarity 40.0%; Pred. No. 7.1;  
Matches 8; Conservative 7; Mismatches 5; Indels 0; Gaps 0;  
QY 9 FVQGLDLSIARLKTSMKFKV 28  
DB 231 FVGRPDVLLVETIVKIFR 250  
RESULT 11  
PANC COREF  
ID PANC COREF STANDARD; PRT; 287 AA.  
AC QGFU6;  
DT 10-OCT-2003 (Rel. 42, Created)  
DT 10-OCT-2003 (Rel. 42, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Pantoate-beta-alanine ligase (EC 6.3.2.1) (pantothenate synthetase)  
DE (Pantoate activating enzyme).  
DE PANC OR CE0115.  
OS Corynebacterium efficiens.  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.  
OX NCBI\_TaxID=152794;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;  
RX MEDLINE=22723752; PubMed=12840036;  
RA Nishio Y., Nakamura Y., Kawabayashi Y., Usuda Y., Kimura E.,  
RA Sugimoto S., Matsui K., Yamagishi A., Kikuchi H., Ikeo K.,  
RA Gojobori T.;  
RT "Comparative complete genome sequence analysis of the amino acid  
RT replacements responsible for the thermostability of Corynebacterium  
RT efficiens".  
RL Genome Res. 13:1572-1579(2003).  
CC -!- CATALYTIC ACTIVITY: ATP + (R)-pantoate + beta-alanine = AMP +  
CC di-phosphate + (R)-pantothenate.  
CC -!- PATHWAY: Pantothenate biosynthesis; last step.  
CC -!- SIMILARITY: Belongs to the pantothenate synthetase family.  
CC  
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CC  
CC EMBL; AP005214; BAC16925.1; ALT\_INIT.  
CC HAMAP; MF 00158; -; 1.  
DR InterPro; IPR003721; Pantoate\_ligase.  
DR Pfam; PF02569; Pantoate\_ligase; 1.  
DR TIGRFAMs; TIGR00018; panC; 1.  
KW Pantothenate biosynthesis; Ligase; Complete proteome.  
SQ SEQUENCE 287 AA; 31266 MW; A5F813159627E7D1 CRC64;  
Query Match 30.7%; Score 47; DB 1; Length 287;  
Best Local Similarity 45.0%; Pred. No. 7.2;  
Matches 9; Conservative 3; Mismatches 8; Indels 0; Gaps 0;  
QY 2 DGGYRKEVQGLDISIARLK 21  
DB 67 DCCDYENYPRQLADADVALLE 86  
RESULT 12  
FA10 RABIT  
ID FA10 RABIT STANDARD; PRT; 490 AA.  
AC Q19045;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Coagulation factor X precursor (SC 3.4.21.6) (Stuart factor).  
DE F10.  
GN Oryctolagus cuniculus (Rabbit).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
OX NCBI\_TaxID=9996;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97256311; PubMed=3101642;  
RA Pendurthi U.R., Anderson K.D., James H.L.;  
RT "Characterization of a full-length cDNA for rabbit factor X.";  
RL Thromb. Res. 85:503-514(1997).  
CC -!- FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that  
CC converts prothrombin to thrombin in the presence of factor Va,  
CC calcium and phospholipid during blood clotting.  
CC -!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Thr and then  
CC Arg-|-Ile bonds in prothrombin to form thrombin.  
CC -!- SUBUNIT: The two chains are formed from a single-chain precursor  
CC by the excision of two Arg residues and are held together by 1 or  
CC more disulfide bonds.  
CC -!- PTM: The vitamin K-dependent, enzymatic carboxylation of some  
CC glutamate residues allows the modified protein to bind calcium (By  
CC similarity).  
CC -!- PTM: N- and O-glycosylated (By similarity).  
CC -!- PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE  
CC INTRINSIC PATHWAY), OR BY FACTOR VIIIA (IN THE EXTRINSIC PATHWAY)  
CC (BY SIMILARITY).  
CC -!- MISCELLANEOUS: Calcium also binds, with stronger affinity to  
CC another site, beyond the GLA domain.  
CC -!- SIMILARITY: Belongs to peptidase family S1.  
CC -!- SIMILARITY: Contains 2 EGF-like domains.  
CC  
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CC  
CC EMBL; AF003200; AAB62542.1; -  
CC HSSP; P00742; 1HCG.  
DR MEROPS; S01.216; -.

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FT 151 BY SIMILARITY
FT 172 INTERCHAIN (BY SIMILARITY).
FT 239 BY SIMILARITY.
FT 244 BY SIMILARITY.
FT 275 BY SIMILARITY.
FT 388 BY SIMILARITY.
FT 413 BY SIMILARITY.
FT 441 BY SIMILARITY.
FT 61 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT 187 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT 205 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT 490 AA; 53965 MW; 3A39FA85AF2A6D11 CRC64;
SQ

Query Match 30.4%; Score 46.5; DB 1; Length 490;
Best Local Similarity 35.7%; Pred. NO. 15;
Matches 10; Conservative 8; Mismatches 7; Indels 3; Gaps 1;

QY 5 RYRFVGG--LDISIALRLKTSKMFVN 29
DB 308 KHRFVKETDFDIARLRLKTPITFRN 335
: : : : : : : : : : : : : : : :
: : : : : : : : : : : : : : : :

RESULT 13
PANC CORGL
ID PANC CORGL STANDARD; PRT; 279 AA.
AC Q9X713;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Pantoate-beta-alanine ligase (EC 6.3.2.1) (Pantothenate synthetase)
DE (Pantoate activating enzyme).
DE PANC OR COLO113.
GN Corynebacterium glutamicum (Brevibacterium flavum).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
NCBI_taxid=1718;
RN [1]
SEQUENCE FROM N.A.
RP STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
RC EDGLINE=99240418; PubMed=10223988;
RX Eggeling L., Sahn H.;
RA "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032."
RT Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
RT panC and genes encoding L-valine synthesis for D-pantothenate
RT overproduction."
RT Appl. Environ. Microbiol. 65:1973-1979(1999).
RN [2]
SEQUENCE FROM N.A.
RP STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
RC Nakagawa S.;
RA "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032."
RT Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
RL -! CATALYTIC ACTIVITY: ATP + (R)-pantoate + beta-alanine = AMP +
CC diphosphate + (R)-pantothenate.
CC -! PATHWAY: Pantothenate biosynthesis; last step.
CC -! SIMILARITY: Belongs to the pantothenate synthetase family.
CC -----
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CC -----
CC EMBL; X96580; CAA65398.1; -.
CC EMBL; AP005274; BAB97506.1; -.
CC PIR; T47120; T47120.
CC HAMAP; MF 00158; -.
CC InterPro; IPR003721; Pantoate ligase.
CC Pfam; PF02569; Pantoate ligase; 1.
CC TIGRFAMs; TIGR00018; panC; 1.
CC Pantothenate biosynthesis; Ligase; Complete proteome.
CC SEQUENCE 279 AA; 29888 MW; EE4CF5EB4198A768 CRC64;
SQ

Query Match 30.1%; Score 46; DB 1; Length 279;

```

Best Local Similarity 45.0%; Pred. No. 10;  
Matches 9; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 2 DCGRYKRVGQDLSIARLK 21  
|||:|:|:|:  
DB 63 DCDYRNYPRQIDADLALLE 82

## RESULT 14

LEUL CANBP  
ID LEUL CANBP STANDARD; PRT; 519 AA.  
AC Q7VQJ6;  
DT 15-MAR-2004 (Rel. 43, Created)  
DT 15-MAR-2004 (Rel. 43, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE 2-isopropylmalate synthase (EC 2.3.3.13) (Alpha-isopropylmalate  
synthase) (Alpha-IPM synthetase).  
GN LEUA OR BFL133.  
OS Candidatus Blochmannia floridanus.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; ant endosymbionts; Candidatus Blochmannia.  
OX NCBI\_TaxID=203907;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22784745; PubMed=12886019;  
RA Gil R., Silva F.J., Zientz E., Delmotte F., Gonzalez-Candelas F.,  
RA Latorre A., Rausell C., Kamerbeek J., Gadau J., Hoelldobler B.,  
RA van Ham R.C.H.J., Gross R., Moya A.;  
RT "The genome sequence of Blochmannia floridanus: comparative analysis  
of reduced genomes".  
RL Proc. Natl. Acad. Sci. U.S.A. 100:9388-9393(2003).  
CC -!- FUNCTION: Catalyzes the condensation of the acetyl group of  
acetyl-CoA with 3-methyl-2-oxobutanoate (2-oxoisovalerate) to form  
3-carboxy-3-hydroxy-4-methylpentanoate (2-isopropylmalate).  
CC -!- CATALYTIC ACTIVITY: Acetyl-CoA + 3-methyl-2-oxobutanoate + H(2)O =  
2-hydroxy-2-isopropylsuccinate + CoA.  
CC -!- PATHWAY: Leucine biosynthesis; first step.  
CC -!- SUBUNIT: Homotrimer (By similarity).  
CC -!- SIMILARITY: Belongs to the alpha-IPM synthetase / homocitrate  
synthase family. Leua 1 subfamily.  
CC  
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL; BX248584; CAD83654.1; -;  
DR HAMAP; MF 01025; -; 1.  
DR InterPro; IPR002034; AIPM/Hcit\_synth.  
DR InterPro; IPR000891; HMGL-like.  
DR InterPro; IPR005671; Leua\_bact\_synth.  
DR Pfam; PF00682; HMGL-like; 1.  
DR TIGRFAMs; TIGR00973; leua\_bact; 1.  
DR PROSITE; PS00815; AIPM\_HOMOCIT\_SYNTH\_1; 1.  
DR PROSITE; PS00816; AIPM\_HOMOCIT\_SYNTH\_2; 1.  
KW Leucine biosynthesis; Transferase; Complete proteome.  
SQ SEQUENCE 519 AA; 58332 MW; 1E03737CEAD8FFD CRC84;

Query Match 30.1%; Score 46; DB 1; Length 519;  
Best Local Similarity 38.5%; Pred. No. 19;  
Matches 10; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

QY 1 CDCGYKRVGQDLSIARLKTSMKF 26

DB 59 CVCGLARCLEKDIDIAEALSAKKF 94

## RESULT 15

YJ16 YEAST  
ID YJ16 YEAST STANDARD; PRT; 604 AA.

P47112;  
DT 01-FEB-1996 (Rel. 33, Created)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DT 01-OCT-1996 (Rel. 34, Last annotation update)  
DE Hypothetical 68.4 kDa protein in SSC1-HYP1 intergenic region.  
GN YJR046W OR J1641.  
OS Saccharomyces cerevisiae (Baker's yeast).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.  
OX NCBI\_TaxID=4932;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=95397595; PubMed=7668047;  
RA Huang M.-B., Chuat J.-C., Galibert F.;  
RT "Analysis of a 42.5 kb DNA sequence of chromosome X reveals three  
tRNA genes and 14 new open reading frames including a gene most  
probably belonging to the family of ubiquitin-protein ligases.";  
RL Yeast 11:775-781(1995).

CC  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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CC

CC EMBL; L36344; AAA88748.1; -;  
DR EMBL; Z49546; CAA89574.1; -;  
DR PIR; S57065; S57065.  
DR GerMOnline; 141879; -;  
DR SGD; S0003807; TAH11.  
DR GO; GO:0005737; C:cytoplasm; IDA.  
DR GO; GO:0005634; C:nucleus; IDA.  
DR GO; GO:0030174; P:DNA replication licensing; IDA.  
KW Hypothetical protein.  
SQ SEQUENCE 604 AA; 68405 MW; 099992C0B3CCA726 CRC64;

Query Match 30.1%; Score 46; DB 1; Length 604;  
Best Local Similarity 60.0%; Pred. No. 22;  
Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 14 DISTARLKTSMKFVK 28

DB 301 ELSILRLQDANKFVK 315

Search completed: March 8, 2004, 12:12:08  
Job time : 5.59912 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 8, 2004, 12:02:31 ; Search time 22.2291 Seconds  
(without alignments)  
411.624 Million cell updates/sec

Title: US-09-600-932-2\_COPY\_119\_147

Perfect score: 153

Sequence: 1 CDCGRYKFKVQGLDISIARLKTSMKFKVN 29

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPREMBL\_25:\*

1: sp\_archaea:\*

2: sp\_bacteria:\*

3: sp\_fungi:\*

4: sp\_human:\*

5: sp\_invertebrate:\*

6: sp\_mammal:\*

7: sp\_mhc:\*

8: sp\_organelle:\*

9: sp\_phase:\*

10: sp\_plant:\*

11: sp\_todent:\*

12: sp\_virus:\*

13: sp\_vertebrate:\*

14: sp\_unclassified:\*

15: sp\_rvirus:\*

16: sp\_bacteriap:\*

17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	153	100.0	277	4 Q9Y6Z7	Q9Y6Z7 homo sapien
2	144	94.1	277	11 Q8CF98	Q8CF98 mus musculus
3	144	94.1	277	11 Q8CIC5	Q8CIC5 mus musculus
4	101	65.0	271	13 Q7T0T0	Q7T0T0 xenopus lae
5	83	54.2	272	11 Q9DC75	Q9DC75 mus musculus
6	80	52.3	268	4 Q7Z6N1	Q7Z6N1 homo sapien
7	80	52.3	271	4 Q8BW88	Q8BW88 homo sapien
8	55	35.9	71	7 Q9GJ67	Q9GJ67 salmo trutt
9	52	34.0	1454	13 Q7ZWK4	Q7ZWK4 xenopus lae
10	50	32.7	282	12 Q91TR4	Q91TR4 tupiaia herp
11	50	32.7	1490	3 Q8TFJ9	Q8TFJ9 debaryomyce
12	49	32.0	149	16 Q884X4	Q884X4 pseudomonas
13	49	32.0	188	2 Q45307	Q45307 bacillus li
14	49	32.0	254	11 P70636	P70636 rattus norv
15	49	32.0	676	11 Q8C855	Q8C855 mus musculus
16	48.5	31.7	1236	5 Q9NXS4	Q9NXS4 leishmania

Q9XZN0 leishmania  
Q9GJ70 salmo trutt  
Q9GJ69 salmo trutt  
Q97MD7 clostridium  
Q83X29 streptomyce  
Q8UZM4 choristoneu  
Q9KAB6 vibrio chol  
Q97QY6 streptococc  
Q9IGH5 oryza sativ  
Q97KW4 clostridium  
Q8ILX4 plasmodium  
Q8DUZ2 streptococc  
Q92CQ8 listeria in  
Q825L5 streptomyce  
Q883E2 pseudomonas  
Q32829 legionella  
Q98JU7 arabidopsis  
Q9GV13 hydra magni  
Q93I76 escherichia  
Q979I4 thermoplasma  
Q8IVX0 homo sapien  
Q14183 homo sapien  
Q7Z590 homo sapien  
P70611 rattus norv  
Q35527 mus musculu  
Q7TNF0 mus musculu  
Q9CJ29 lactococcus  
Q9GVA1 stvela clav  
P78720 orpinomyces

#### ALIGNMENTS

RESULT 1

Q9Y6Z7 ID Q9Y6Z7 PRELIMINARY; PRT; 277 AA.  
AC Q9Y6Z7;  
DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Collectin 34.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
EX MEDLINE=99240768; PubMed=10224141;  
RA Ohnani K., Suzuki Y., Eda S., Kawai T., Kase T., Yamazaki H.,  
RA Keshi H., Sakai Y., Fukuo A., Sakamoto T., Wakamiya N.;  
RT "Molecular cloning of a novel collectin from liver (CL-L1).";  
RL J. Biol. Chem. 274:13681-13689(1999).  
DR EMBL; AB002631; BAA81747.1; -.  
DR HSSP; P19999; 2MSB.  
DR Genew; HGNC:2220; COLC10.  
DR GO; GO:0005737; C:cytoplasm; TAS.  
DR GO; GO:0005530; F:lectin; TAS.  
DR InterPro; IPR008160; Collagen.  
DR InterPro; IPR001304; Lectin\_C.  
DR Pfam; PF01391; Collagen; 1.  
DR Pfam; PF00059; Lectin\_C; 1.  
DR SMART; SM00034; CLACT; 1.  
DR PROSITE; PS00615; C-TYPE LECTIN 1; 1.  
DR PROSITE; PSS0041; C-TYPE LECTIN 2; 1.  
SQ SEQUENCE 277 AA; 30733 MW; 9736861CEBDCSC25 CRC64;

Query Match 100.0%; Score 153; DB 4; Length 277;  
Best Local Similarity 100.0%; Pred. No. 5.8e-16;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDCGRYKFKVQGLDISIARLKTSMKFKVN 29

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Db 119 CDCGRYKRVGQLDISARLKTSMKFVN 147
RESULT 2
Q8CF98 PRELIMINARY; PRT; 277 AA.
AC Q8CF98;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Collectin-11.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RX MEDLINE=2233327; PubMed=1450124;
RA Kawai T., Suzuki Y., Eda S., Kase T., Ohtani K., Sakai Y., Keshi H.,
RA Fukuchi A., Sakamoto T., Nozaki M., Copeland N.G., Jenkins N.A.,
RA Wakamiya N.;
RT "Molecular Cloning of Mouse Collectin Liver 1.";
RL BIOSIS: Biotechnol. Biochem. 66:2134-2145(2002).
DR ENBL; AB018429; BAC53954.1; --
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR008160; Collagen.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF01391; Collagen; 1.
DR Pfam; PF00059; lectin.c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
DR PROSITE; PS00041; C_TYPE_LLECTIN_2; 1.
SQ SEQUENCE 277 AA; 30524 MW; 98C743A2B07A2872 CRC64;

Query Match 94.1%; Score 144; DB 11; Length 277;
Best Local Similarity 89.7%; Pred. No. 1.6e-14;
Matches 26; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CDCGRYKRVGQLDISARLKTSMKFVN 29
Db 119 CDCGRYKRVGQLDISARLKTSMKFVN 147

RESULT 3
Q8C1C5 PRELIMINARY; PRT; 277 AA.
AC Q8C1C5;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Collectin 34 homolog.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium.
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR ENBL; AK028423; BAC25941.1; --
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR008160; Collagen.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF01391; Collagen; 1.
DR Pfam; PF00059; lectin.c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
```

```
DR PROSITE; PS00041; C_TYPE_LLECTIN_2; 1.
SQ SEQUENCE 277 AA; 30510 MW; 94EF23A2E5404872 CRC64;

Query Match 94.1%; Score 144; DB 11; Length 277;
Best Local Similarity 89.7%; Pred. No. 1.6e-14;
Matches 26; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CDCGRYKRVGQLDISARLKTSMKFVN 29
Db 119 CDCGRYKRVGQLDISARLKTSMKFVN 147

RESULT 4
Q7T0T0 PRELIMINARY; PRT; 271 AA.
AC Q7T0T0;
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Hypothetical protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22341132; PubMed=12454917;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RA "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22389257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko I., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalls D.S., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Klein S., Strausberg R.;
RA Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR ENBL; BC056052; AAH56052.1; --
RW Hypothetical protein.
SQ SEQUENCE 271 AA; 29334 MW; 587129273C476AE2 CRC64;

Query Match 66.0%; Score 101; DB 13; Length 271;
Best Local Similarity 58.6%; Pred. No. 1.1e-07;
Matches 17; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 CDCGRYKRVGQLDISARLKTSMKFVN 29
Db 119 CDCGRYKRVGQLDISARLKTSMKFVN 147
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Db 113 CECGQLKRAVGEMDIQVAQLATEYKFKVN 141

RESULT 5  
Q9DC75 PRELIMINARY; PRT; 272 AA.

AC Q9DC75; (1)  
DT 01-JUN-2001 (TRENBLrel. 17, Created)  
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)  
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)  
DE 101000IH6RIK protein.  
GN 101000IH6RIK.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX STRAIN=CS7BL/6J; TISSUE=Heart;  
RC MEDLINE=21085660; PubMed=11217851;  
RA Kawai J., Shinagawa A., Shibata Y., Konno H., Adachi S., Fukuda S.,  
RA Arakawa T., Hara A., Fukunishi Y., Kondo S., Yamazaki I.,  
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamazaki I.,  
RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,  
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,  
RA Schriml L.M., Staib F., Suzuki R., Tomita M., Wagner L., Washio T.,  
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
RA Blake J., Roffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
RA Brownstein M.J., Bul C., Fletcher C., Fujita M., Gariboldi M.,  
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
RA Lyons P., Marchionni L., Mashima J., Rodriguez I., Sakamoto N.,  
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,  
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,  
RA Hayaishizaki Y.,  
RT Functional annotation of a full-length mouse cDNA collection."  
RL Nature 409:685-690(2001).  
DR EMBL; AK003121; BAB22581.1; -.  
DR HSSP; P22897; LEGG.  
DR MGD; MGI:1918943; 101000IH6RIK.  
DR GO; GO:0005529; F:sugar binding; IEA.  
DR InterPro; IPR008160; Collagen.  
DR InterPro; IPR001304; LECTIN\_C.  
DR Pfam; PF01391; Collagen; 1.  
DR Pfam; PF00059; lectin c; 1.  
DR SMART; SM00034; CLECT; 1.  
DR PROSITE; PS00615; C-TYPE LECTIN 1; 1.  
DR PROSITE; PS50041; C-TYPE LECTIN 2; 1.  
SQ SEQUENCE 272 AA; 28975 MW; DE471493CD16B95 CRC64;

Query Match 54.2%; Score 83; DB 11; Length 272;  
Best Local Similarity 41.4%; Pred. No. 8e-05;  
Matches 12; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

QY 1 CDGGRYKRVGOLDISIARLKTSMKFKVN 29  
Db 114 CECGQLKRAVGEMDQVQTTLKFKVN 142

RESULT 6  
Q7Z6N1 PRELIMINARY; PRT; 268 AA.

AC Q7Z6N1; (1)  
DT 01-OCT-2003 (TRENBLrel. 25, Created)  
DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)  
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)  
DE MGC3279 protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klautner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Franke C.,  
RA Raha S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences".  
RT Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX TISSUE=Brain;  
RC Strausberg R.;  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC009951; AAH09951.1; -.  
SQ SEQUENCE 268 AA; 29005 MW; 30C30CC8258AA9B7 CRC64;

Query Match 52.3%; Score 80; DB 4; Length 268;  
Best Local Similarity 37.9%; Pred. No. 0.00024;  
Matches 11; Conservative 11; Mismatches 7; Indels 0; Gaps 0;

QY 1 CDGGRYKRVGOLDISIARLKTSMKFKVN 29  
Db 110 CECGQLKRAVGEMDQVQSLTSLKFKVN 138

RESULT 7  
Q9BWP8 PRELIMINARY; PRT; 271 AA.

AC Q9BWP8; (1)  
DT 01-JUN-2001 (TRENBLrel. 17, Created)  
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)  
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RA Strausberg R.;  
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC000078; AAH00078.1; -.  
DR HSSP; P22897; LEGG.  
DR GO; GO:0005529; F:sugar binding; IEA.  
DR InterPro; IPR008160; Collagen.  
DR InterPro; IPR001304; LECTIN\_C.  
DR Pfam; PF01391; Collagen; 1.  
DR Pfam; PF00059; lectin c; 1.  
DR SMART; SM00034; CLECT; 1.  
DR PROSITE; PS00615; C-TYPE LECTIN 1; 1.  
DR PROSITE; PS50041; C-TYPE LECTIN 2; 1.  
KW Hypothetical protein.  
SQ SEQUENCE 271 AA; 28665 MW; A14A248CE41DB340 CRC64;

Query Match 52.3%; Score 80; DB 4; Length 271;

Best Local Similarity 37.9%; Pred. No. 0.00024;  
Matches 11; Conservative 11; Mismatches 7; Indels 0; Gaps 0;

QY 1 CDCGRYKRVGQDLSIARLKTSMKFKVN 29  
Db 113 CBCSOLRAIGMDNQVSLTSELAIFKN 141

RESULT 8  
Q9GJ67 PRELIMINARY; PRT; 71 AA.  
AC Q9GJ67;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE MHC class II alpha chain (Fragment).  
GN SAIR-DAA.  
OS Salmo trutta (Brown trout).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.  
OX NCBI\_TaxID=8032;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Stet R.J.M., Jordan W.C.;  
RT "Class II alpha chain in brown trout (Salmo trutta).";  
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ293954; CAC08191.1;  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0006955; P:immune response; IEA.  
DR InterPro; IPR001003; MHC\_II\_alpha.  
DR Pfam; PF00993; MHC\_II\_alpha; 1.  
FT NON TER 1  
FT NON TER 71  
SQ SEQUENCE 71 AA; 7667 MW; C00A0CCA0708BEE0 CRC64;

Query Match 35.9%; Score 55; DB 7; Length 71;  
Best Local Similarity 46.2%; Pred. No. 0.56;  
Matches 12; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 4 GRYKRVGQDLSIARLKTSMKFKVN 29  
Db 43 GAVEQAVGELGVCKANLATSIKAYKN 68

RESULT 9  
Q7ZWK4 PRELIMINARY; PRT; 1454 AA.  
AC Q7ZWK4;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Similar to plectin (Fragment).  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;  
OC Xenopodinae; Xenopus.  
OX NCBI\_TaxID=8355;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA TISSUE=Embryo;  
RC Klein S., Strausberg R.;  
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC048220; AAH48220.1;  
DR GO; GO:0003779; F:actin binding; IEA.  
DR InterPro; IPR001589; Actbind actnin.  
DR InterPro; IPR001715; Calponin-like.  
DR InterPro; IPR002017; Spectrin.  
DR Pfam; PF00307; Ch; 2.  
DR Pfam; PF00435; spectrin; 1.  
DR SMART; SM00033; CH; 2.  
DR SMART; SM00150; SPEG; 5.  
DR PROSITE; PS00019; ACTININ\_1; 1.

DR PROSITE; PS00021; CH; 2.  
FT NON TER 1454 1454  
SQ SEQUENCE 1454 AA; 170240 MW; EA3DDB6ECD3BDAC9 CRC64;

Query Match 34.0%; Score 52; DB 13; Length 1454;  
Best Local Similarity 40.9%; Pred. No. 41;  
Matches 9; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY 4 GRYKRVGQDLSIARLKTSMK 25  
Db 590 GSYQEYLGKLDLQYAKLNSK 611

RESULT 10  
Q91TR4 PRELIMINARY; PRT; 282 AA.  
ID Q91TR4;  
AC Q91TR4;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE T29.3.  
OS Tupiaia herpesvirus.  
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
OC Betaherpesvirinae.  
OX NCBI\_TaxID=10397;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=2;  
RX MEDLINE=21211637; PubMed=11312357;  
RA Bahr U., Darai G.;  
RT "Analysis and Characterization of the Complete Genome of Tupiaia (Tree Shrew) Herpesvirus";  
RL J. Virol. 75:4854-4870(2001).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=2;  
RA Darai G., Bahr U.;  
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF281817; AAK57073.1;  
SQ SEQUENCE 282 AA; 28737 MW; 6166B8DBF7981864 CRC64;

Query Match 32.7%; Score 50; DB 12; Length 282;  
Best Local Similarity 39.1%; Pred. No. 15;  
Matches 9; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY 6 YRKRVGQDLSIARLKTSMKFKV 28  
Db 209 WAEFFGKCSLSIARLKGFEYVK 231

RESULT 11  
Q8TFJ9 PRELIMINARY; PRT; 1490 AA.  
ID Q8TFJ9;  
AC Q8TFJ9;  
DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Polypyrroline.  
GN GAG.  
OS Debaryomyces hansenii var. hansenii.  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Debaryomycetes.  
OX NCBI\_TaxID=58641;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CBS767; TRANSPOSON=LTR-retrotransposon Tdh5;  
RA Neuveglise C., Feldmann H., Bon E., Gaillardin C., Casaregola S.;  
RT "Genomic evolution of the LTR-retrotransposons in hemiascomycetous yeasts";  
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ439552; CAD29538.1;  
DR GO; GO:0003677; F:DNA binding; IEA.  
DR GO; GO:0003723; F:RNA binding; IEA.



DR GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.  
DR GO; GO:0016740; F:transferase activity; IEA.  
DR GO; GO:006310; P:DNA recombination; IEA.  
DR GO; GO:0008278; P:RNA dependent DNA replication; IEA.  
DR InterPro; IPR001894; RVB.  
DR InterPro; IPR000477; RVFse.  
DR InterPro; IPR001878; Znf\_CCHC.  
DR Pfam; PF00665; rve; 1.  
DR Pfam; PF00078; rvt; 1.  
DR Pfam; PF00098; zf-CCHC; 1.  
DR PRINTS; PR00939; C2HCZNFINGER.  
DR SMART; SM00343; Znf\_C2HC; 1.  
DR PROSITE; PS0158; ZF\_CCHC; 1.  
KW RNA-directed DNA polymerase; Transferase.  
SQ SEQUENCE 1490 AA; 166461 MW; 2EALB73403FC967B CRC64;

Query Match 32.7%; Score 50; DB 3; Length 1490;  
Best Local Similarity 34.6%; Pred.No. 88;  
Matches 9; Conservative 6; Mismatches 11; Indels 0; Gaps 0;

QY 1 CDCGRYKRVGQLDISIARLKTSMKF 26  
||| ||| ||| : : : : :  
DB 1262 CDATYRSLVGKLFPASTVTRTDIAY 1287

RESULT 12  
Q884X4 PRELIMINARY; PRT; 149 AA.  
AC Q884X4;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Flagellar protein FljJ, putative.  
GN PSPT01962.  
OS Pseudomonas syringae (pv. tomato).  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
OC Pseudomonadaceae; Pseudomonas.  
OX NCBI\_TaxID=323;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=DC3000;  
RA Buell R., Joardar V., Khouri H., Fedorova N., Tran B., Russell D.,  
Berry K., Utterback T., Van Aken S., Feldblyum T., Gwin M.,  
Dodson R., DeBoy R., Durkin A., Kolonay J., Madupu R., Daugherty S.,  
Brinkac L., Beanan M., Haft D., Selengut J., Nelson W., Davidson T.,  
White O., Fraser C., Collier A.;  
RT "Complete sequence of Pseudomonas syringae";  
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
DR ENBL; AB016862; AA055480.1; -.  
DR TIGR; PSPT01962; -.  
KW Complete proteome.  
SQ SEQUENCE 149 AA; 17515 MW; 210720F49E407291 CRC64;

Query Match 32.0%; Score 49; DB 16; Length 149;  
Best Local Similarity 34.6%; Pred.No. 11;  
Matches 8; Conservative 10; Mismatches 5; Indels 0; Gaps 0;

QY 6 YRKRFVGLDISIARLKTSMKFVK 28  
||| ||| ||| : : : : :  
DB 71 YQRFSLQDVAQAQYKSLWEHK 93

RESULT 13  
Q45307 PRELIMINARY; PRT; 188 AA.  
AC Q45307;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Saz divib (Fragment).  
OS Bacillus licheniformis.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
OX NCBI\_TaxID=1402;

RN SEQUENCE FROM N.A.  
RP STRAIN=5A2;  
RC MEDLINE=94374713; PubMed=8088553;  
EX Harry E.J., Partridge S.R., Weiss A.S., Wake R.G.;  
RT "Conservation of the 188 divB gene in Bacillus subtilis W23 and B.  
RT licheniformis, and evidence for homology to ftsQ of Escherichia  
RT coli.";  
RL Gene 147:85-89(1994).  
DR EMBL; U01958; AAA57245.1; -.  
DR PIR; I40222; I40222.  
FT NON\_TER 188  
SQ SEQUENCE 188 AA; 21681 MW; 7D544902412E1774 CRC64;

Query Match 32.0%; Score 49; DB 2; Length 188;  
Best Local Similarity 37.5%; Pred.No. 14;  
Matches 9; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 2 DCGYRKRVGQLDISIARLKTSMK 25  
||| ||| ||| : : : : :  
DB 90 DVERYRMFVGEGIGQGGIKVTLK 113

RESULT 14  
P70636 PRELIMINARY; PRT; 254 AA.  
AC P70636;  
DT 01-FEB-1997 (TrEMBLrel. 02, Created)  
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Laminin chain (Fragment).  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Buffalo; TISSUE=Liver;  
RX MEDLINE=98085771; PubMed=9417868;  
RA Seebacher T., Medina J.L., Bade B.G.;  
RT "Laminin alpha5, a major transcript of normal and malignant rat liver  
RT epithelial cells, is differentially expressed in developing and adult  
RT liver.";  
RL Exp. Cell Res. 237:70-76(1997).  
DR EMBL; Y08882; CAA70093.1; -.  
DR InterPro; IPR008985; ConA\_like\_lec\_gl.  
FT NON\_TER 1  
FT NON\_TER 254  
SQ SEQUENCE 254 AA; 27708 MW; 68C5837F7B83414E CRC64;

Query Match 32.0%; Score 49; DB 11; Length 254;  
Best Local Similarity 43.5%; Pred.No. 19;  
Matches 10; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 4 GRYKRVGQLDISIARLKTSMKF 26  
||| ||| ||| : : : : :  
DB 97 GRVKLIQAARSANKVKSMKF 119

RESULT 15  
Q8C8S5 PRELIMINARY; PRT; 676 AA.  
AC Q8C8S5;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Plectin 1 (Fragment).  
GN PLEC1.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]

RP SEQUENCE FROM N.A.  
RC STRAIN=CS7BL/6J; TISSUE=Retina;  
RX MEDLINE=22354683; PubMed=12466851;  
RA The FANTOM Consortium,  
RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RL Nature 420:563-573 (2002).  
RL 60,770 full-length cDNAs.";  
DR EMBL; AK044559; BAC31980.1; -.  
DR MGD; MGI:1277961; Plecl.  
DR GO; GO:003779; F-actin binding; IEA.  
DR InterPro; IPR001599; Actbind\_actinin.  
DR InterPro; IPR001715; Calponin-like.  
DR InterPro; IPR002017; Spectrin.  
DR Pfam; PF00307; CH; 2.  
DR SMART; SM00033; CH; 2.  
DR SMART; SM00150; SPEC; 1.  
DR PROSITE; PS00019; ACTININ\_1; 1.  
DR PROSITE; PS0021; CH; 2.  
FT NON\_TER 676  
SQ SEQUENCE 676 AA; 77580 MW; 6DA7D8815CAB6C70 CRC64;  
  
Query Match 32.0%; Score 49; DB 11; Length 676;  
Best Local Similarity 45.5%; Pred. No. 55;  
Matches 10; Conservative 4; Mismatches 8; Indels 0; Gaps 0;  
  
QY 4 GYRKFVQGLDISIARLKTSMK 25  
DB 631 GAYRDCLGREDLQYAKLNSK 652  
  
Search completed: March 8, 2004, 12:15:13  
Job time : 23.2291 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 8, 2004, 12:11:31 ; Search time 10.4758 Seconds  
(without alignments)  
584.534 Million cell updates

Title: US-09-600-932-2 COPY 119 147

Perfect score: 153  
Sequence: 1 CDCGRYKFGQLDISIARLKTSMKFVN 29

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 809742 seqs, 211153259 residues

Total number of hits satisfying chosen parameters: 809742

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 BU

Database : Published Applications

1: /cgn2\_6/ptodata/2/pubpaa/  
2: /cgn2\_5/ptodata/2/pubpaa/  
3: /cgn2\_4/ptodata/2/pubpaa/

2: /cgm2\_6/prodata/2/pubpaa/pc1\_NEW\_PUB.pcp.\*  
3: /cgm2\_6/prodata/2/pubpaa/US06\_NEW\_PUB.pcp.\*  
4: /cgm2\_6/prodata/2/pubpaa/US06\_PUBCOMB.pcp.\*  
5: /cgm2\_6/prodata/2/pubpaa/US07\_NEW\_PUB.pcp.\*  
6: /cgm2\_6/prodata/2/pubpaa/PC1US\_PUBCOMB.pcp.\*  
7: /cgm2\_6/prodata/2/pubpaa/US08\_NEW\_PUB.pcp.\*  
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15: /cgm2\_6/prodata/2/pubpaa/US10C\_PUBCOMB.pcp.\*  
16: /cgm2\_6/prodata/2/pubpaa/US10\_NEW\_PUB.pcp.\*  
17: /cgm2\_6/prodata/2/pubpaa/US60\_NEW\_PUB.pcp.\*  
18: /cgm2\_6/prodata/2/pubpaa/US60\_PUBCOMB.pcp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query %		Length	DB	ID	Description
		Match					
1	153	100.0	159	14	US-10-358-105-14		Sequence 14, Appl
2	153	100.0	277	9	US-09-978-395A-97		Sequence 97, Appl
3	153	100.0	277	9	US-09-978-697-97		Sequence 97, Appl
4	153	100.0	277	9	US-09-978-192A-97		Sequence 97, Appl
5	153	100.0	277	9	US-09-999-832A-97		Sequence 97, Appl
6	153	100.0	277	10	US-09-978-189-97		Sequence 97, Appl
7	153	100.0	277	10	US-09-978-608A-97		Sequence 97, Appl
8	153	100.0	277	10	US-09-978-588A-97		Sequence 97, Appl
9	153	100.0	277	10	US-09-978-191A-97		Sequence 97, Appl
10	153	100.0	277	10	US-09-978-403A-97		Sequence 97, Appl
11	153	100.0	277	10	US-09-978-564A-97		Sequence 97, Appl
12	153	100.0	277	10	US-09-999-833A-97		Sequence 97, Appl
13	153	100.0	277	10	US-09-981-915A-97		Sequence 97, Appl
14	153	100.0	277	10	US-09-978-824-97		Sequence 97, Appl
15	153	100.0	277	10	US-09-918-588A-97		Sequence 97, Appl

16	153	100.0	277	10	US-09-978-433A-97	Sequence 97, App1
17	153	100.0	277	10	US-09-978-133A-97	Sequence 97, App1
18	153	100.0	277	10	US-09-999-830A-97	Sequence 97, App1
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20	153	100.0	277	10	US-09-978-187B-97	Sequence 97, App1
21	153	100.0	277	10	US-09-978-643A-97	Sequence 97, App1
22	153	100.0	277	10	US-09-978-375A-97	Sequence 97, App1
23	153	100.0	277	10	US-09-978-298A-97	Sequence 97, App1
24	153	100.0	277	10	US-09-978-188A-97	Sequence 97, App1
25	153	100.0	277	10	US-09-978-681A-97	Sequence 97, App1
26	153	100.0	277	10	US-09-978-134A-97	Sequence 97, App1
27	153	100.0	277	10	US-09-999-829A-97	Sequence 97, App1
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29	153	100.0	277	10	US-09-978-544A-97	Sequence 97, App1
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31	153	100.0	277	10	US-09-978-802A-97	Sequence 97, App1
32	153	100.0	277	13	US-10-052-586-100	Sequence 100, App
33	153	100.0	277	14	US-10-174-580-100	Sequence 100, App
34	153	100.0	277	14	US-10-176-758-100	Sequence 100, App
35	153	100.0	277	14	US-10-175-737-100	Sequence 100, App
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39	153	100.0	277	14	US-10-176-482-100	Sequence 100, App
40	153	100.0	277	14	US-10-176-757-100	Sequence 100, App
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## ALIGNMENTS

## RESULT 1

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US-10-258-105-14
; Sequence 14, Application US/10258105
; Publication No. US20030158382A1
; GENERAL INFORMATION:
; APPLICANT: Wakamiya et al.
; TITLE OF INVENTION: No. US20030158382A1el Collectin
; FILE REFERENCE: 190367/38785
; CURRENT APPLICATION NUMBER: US/10/2556,105
; CURRENT FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: PCT/JP01/03468
; PRIOR FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: JP 2000-120358
; PRIOR FILING DATE: 2000-04-21
; NUMBER OF SEQ IDS NOS: 61
; SEQ ID NO 14
; LENGTH: 159
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Known CRD amino acid sequence of
; OTHER INFORMATION: for searching EST data base.
US-10-258-105-14

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1  NUMBER OF SEQUENCES: 1
2  NUMBER OF SEQ ID NOS: 61
3  /
4  SEQ ID NO 1:
5  /
6  LENGTH: 159
7  /
8  TYPE: PRT
9  /
10 ORGANISM: Homo sapiens
11 /
12 FEATURES:
13 /
14 OTHER INFORMATION: Known CRD amino acid sequence of reported CL-L1 which was employed
15 /
16 OTHER INFORMATION: for searching EST data base.
17 /

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Query Match      100.0%; Score 153; DB 14; Length 159;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 CDCGRYKFGQLDISIARLKTSMKFKVN 29  
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Db 1 CDCGRYKFGQLDISIARLKTSMKFKVN 29

RESULT 2  
US-09-978-235A-97  
; Sequence 97, Application US/09978295A  
; Patent No. US20020156005A1  
; GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kiljavin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2630PIC11  
CURRENT APPLICATION NUMBER: US/09/978,295A  
CURRENT FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: 09/918595  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066364  
PRIOR FILING DATE: 1997-11-21  
PRIOR APPLICATION NUMBER: 60/077450  
PRIOR FILING DATE: 1998-03-10  
PRIOR APPLICATION NUMBER: 60/077632  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077641  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077649  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077791  
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PRIOR FILING DATE: 1998-04-29

APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
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APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2630PIC27  
CURRENT APPLICATION NUMBER: US/09/978,697  
CURRENT FILING DATE: 2001-10-16  
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PRIOR FILING DATE: 2001-07-30  
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Query Match 100.0%; Score 153; DB 9; Length 277;  
Best Local Similarity 100.0%; Pred. No. 2e-16; 0; Mismatches 0; Indels 0; Gaps 0;  
Matches 29; Conservative 0;

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Sequence 97 Application US/09978697  
Patent No. US20020169284A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnovers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen



1	APPLICANT: Gurney, Austin L.	1	PRIOR FILING DATE: 1998-03-31
2	APPLICANT: Hillan, Kenneth J	2	PRIOR APPLICATION NUMBER: 60/080327
3	APPLICANT: Kijavin, Ivar J.	3	PRIOR FILING DATE: 1998-04-01
4	APPLICANT: Kuo, Sophia S.	4	PRIOR APPLICATION NUMBER: 60/080328
5	APPLICANT: Napier, Mary A.	5	PRIOR FILING DATE: 1998-04-01
6	APPLICANT: Pan, James	6	PRIOR APPLICATION NUMBER: 60/080333
7	APPLICANT: Paoni, Nicholas F.	7	PRIOR FILING DATE: 1998-04-01
8	APPLICANT: Roy, Margaret Ann	8	PRIOR APPLICATION NUMBER: 60/080334
9	APPLICANT: Shelton, David L.	9	PRIOR FILING DATE: 1998-04-01
10	APPLICANT: Stewart, Timothy A.	10	PRIOR APPLICATION NUMBER: 60/081070
11	APPLICANT: Tumas, Daniel	11	PRIOR FILING DATE: 1998-04-08
12	APPLICANT: Williams, P. Mickey	12	PRIOR APPLICATION NUMBER: 60/081049
13	APPLICANT: Wood, William I.	13	PRIOR FILING DATE: 1998-04-08
14	TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic	14	PRIOR APPLICATION NUMBER: 60/081071
15	TITLE OF INVENTION: Acids Encoding the Same	15	PRIOR FILING DATE: 1998-04-08
16	FILE REFERENCE: P2630PIC9	16	PRIOR APPLICATION NUMBER: 60/081195
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Query Match 100.0%; Score 153; DB 9; Length 277;

Best Local Similarity 100.0%; Pred. No. 2e-16;

Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDGGRKFKVQGLDLSIARLTKSMKFKVN 29  
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## RESULT 5

US-09-999-832A-97

Sequence 97, Application US/09999832A

Publication No. US20020192706A1

## GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
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APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2630PIC63  
CURRENT FILING DATE: 2001-10-24  
PRIOR APPLICATION NUMBER: US/09/999,832A  
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;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 153; DB 9; Length 277;  
Best Local Similarity 100.0%; Pred. No. 2e-16;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 CDCGRYKFGQLDISIARLKTSMKPFVN 29  
D6 119 CDCGRYKFGQLDISIARLKTSMKPFVN 147

RESULT 6  
US-09-978-189-97  
; Sequence 97, Application US/09978189  
; Publication No. US20030004102A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James;  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tamas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

;; TITLE OF INVENTION: Acids Encoding the Same  
;; FILE REFERENCE: P2630P.C7  
;; CURRENT APPLICATION NUMBER: US/09/978,189  
;; CURRENT FILING DATE: 2001-10-15  
;; PRIOR APPLICATION NUMBER: 09/918585  
;; PRIOR FILING DATE: 2001-07-30  
;; PRIOR APPLICATION NUMBER: 60/062250  
;; PRIOR FILING DATE: 1997-10-17  
;; PRIOR APPLICATION NUMBER: 60/064249  
;; PRIOR FILING DATE: 1997-11-03  
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;; PRIOR APPLICATION NUMBER: 60/077450  
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;; PRIOR FILING DATE: 1998-04-27  
;; PRIOR APPLICATION NUMBER: 60/083322  
;; PRIOR FILING DATE: 1998-04-28  
;; PRIOR APPLICATION NUMBER: 60/083392  
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;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085580  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085573  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085704  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 153; DB 10; Length 277;  
Best Local Similarity 100.0%; Pred. No. 2e-16;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDCGRRKFKVQGLDISIARLKTSMKFVKV 29  
Db 119 CDCGRRKFKVQGLDISIARLKTSMKFVKV 147

RESULT 7  
US-09-978-608A-97  
; Sequence 97, Application US/09978608A  
; Publication No. US20030045462A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Deenoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James;  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2630P1C22  
; CURRENT APPLICATION NUMBER: US/09/978,608A  
; NUMBER OF SEQ ID NOS: 624  
; Prior Application removed - See File Wrapper or Palm  
; SEQ ID NO 97

;; LENGTH: 277  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-09-978-608A-97

Query Match 100.0%; Score 153; DB 10; Length 277;  
Best Local Similarity 100.0%; Pred. No. 2e-16;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDCGRRKFKVQGLDISIARLKTSMKFVKV 29  
Db 119 CDCGRRKFKVQGLDISIARLKTSMKFVKV 147

RESULT 8  
US-09-978-585A-97  
; Sequence 97, Application US/09978585A  
; Publication No. US20030049633A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Deenoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: KJavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James;  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2630P1C15  
; CURRENT APPLICATION NUMBER: US/09/978,585A  
; NUMBER OF SEQ ID NOS: 624  
; Prior Application removed - See File Wrapper or Palm  
; SEQ ID NO 97  
; LENGTH: 277  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-978-585A-97

Query Match 100.0%; Score 153; DB 10; Length 277;  
Best Local Similarity 100.0%; Pred. No. 2e-16;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDCGRRKFKVQGLDISIARLKTSMKFVKV 29  
Db 119 CDCGRRKFKVQGLDISIARLKTSMKFVKV 147

RESULT 9  
US-09-978-191A-97  
; Sequence 97, Application US/09978191A  
; Publication No. US20030050239A1  
; GENERAL INFORMATION:



;; PRIOR APPLICATION NUMBER: 60/083554  
;; PRIOR FILING DATE: 1998-04-29  
;; PRIOR APPLICATION NUMBER: 60/083558  
;; PRIOR FILING DATE: 1998-04-29  
;; PRIOR APPLICATION NUMBER: 60/083559  
;; PRIOR FILING DATE: 1998-04-29  
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;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 153; DB 10; Length 277;  
Best Local Similarity 100.0%; Pred. No. 2e-16;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2y 1 CDCGRYKFGQLDISIAIKNTSMKFKVN 29  
|||  
db 119 CDCGRYKFGQLDISIAIKNTSMKFKVN 147  
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## RESULT 10

JS-09-978-403A-97  
; Sequence 97, Application US/09978403A  
; Publication No. US20030050240A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen

;; APPLICANT: Fong, Sherman  
;; APPLICANT: Gao, Wei-Qiang  
;; APPLICANT: Gerber, Hanspeter  
;; APPLICANT: Gerritsen, Mary E.  
;; APPLICANT: Goddard, Audrey  
;; APPLICANT: Godowski, Paul J.  
;; APPLICANT: Grimaldi, J. Christopher  
;; APPLICANT: Gurney, Austin L.  
;; APPLICANT: Hillan, Kenneth J.  
;; APPLICANT: Kijavini, Ivar J.  
;; APPLICANT: Kuo, Sophia S.  
;; APPLICANT: Napier, Mary A.  
;; APPLICANT: Paoni, Nicholas F.  
;; APPLICANT: Roy, Margaret Ann  
;; APPLICANT: Shelton, David L.  
;; APPLICANT: Stewart, Timothy A.  
;; APPLICANT: Tumas, Daniel  
;; APPLICANT: Williams, P. Mickey  
;; APPLICANT: Wood, William I.  
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
;; FILE OF INVENTION: Acids Encoding the Same  
;; FILE REFERENCE: P2630P1C17  
;; CURRENT APPLICATION NUMBER: US/09/978,403A  
;; CURRENT FILING DATE: 2002-03-19  
;; PRIOR APPLICATION NUMBER: 09/918585  
;; PRIOR FILING DATE: 2001-07-30  
;; PRIOR APPLICATION NUMBER: 60/062250  
;; PRIOR FILING DATE: 1997-10-17  
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;; PRIOR APPLICATION NUMBER: 60/084639  
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;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 153; DB 10; Length 277;  
Best Local Similarity 100.0%; Pred. No. 2e-16; Indels 0; Gaps 0;  
Matches 29; Conservative 0; Mismatches 0

QY 1 CDCGRYKFCQDLSIARLKTSMKFKVN 29  
Db 119 CDCGRYKFCQDLSIARLKTSMKFKVN 147

RESULT 11  
US-09-978-564A-97  
; Sequence 97, Application US/09978564A  
; Publication No. US20030050241A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Deanovs, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kilavin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2630P1C25  
CURRENT APPLICATION NUMBER: US/09/978,564A  
CURRENT FILING DATE: 2001-10-16  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
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Query Match 100.0%; Score 153; DB 10; Length 277;

Best Local Similarity 100.0%; Pred. No. 2e-16;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDCGRYKRVGVGLDTSIARLKTSMKFVN 29  
DB 119 CDCGRYKRVGVGLDTSIARLKTSMKFVN 147

RESULT 12  
US-09-999-833A-97  
Sequence 97, Application US/09999833A  
Publication No. US20030054405A1

GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.

;; APPLICANT: Roy, Margaret Ann  
;; APPLICANT: Shelton, David L.  
;; APPLICANT: Stewart, Timothy A.  
;; APPLICANT: Tumas, Daniel  
;; APPLICANT: Williams, P. Mickey  
;; APPLICANT: Wood, William I.  
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
;; FILE OF INVENTION: Acids Encoding the Same  
;; FILE REFERENCE: P2630P1665  
;; CURRENT APPLICATION NUMBER: US/09/999,833A  
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;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 153; DB 10; Length 277;  
Best Local Similarity 100.0%; Pred. No. 2e-16; Indels 0; Gaps 0;  
Matches 29; Conservative 0; Mismatches 0

Qy 1 CDCGRRKFKVQGLDISIARLKTSMKFKVN 29  
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Db 119 CDCGRRKFKVQGLDISIARLKTSMKFKVN 147  
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RESULT 13  
US-09-981-915A-97  
; Sequence 97, Application US/09981915A  
; Publication No. US20030054986A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnovers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
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; APPLICANT: Grimaldi, J. Christopher  
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; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kijavini, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
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; APPLICANT: Shelton, David L.  
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; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

;; TITLE OF INVENTION: Acids Encoding the Same  
;; FILE REFERENCE: P2630FIC12  
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;; PRIOR FILING DATE: 1998-05-15  
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;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 153; DB 10; Length 277;

Best Local Similarity 100.0%; Pred. No. 2e-16; Mismatches 0; Indels 0; Gaps 0;

2y 1 CDCGVRKRVQGLDISIARLKTSMKFKVN 29  
db 119 CDCGVRKRVQGLDISIARLKTSMKFKVN 147

## RESULT 14

US-09-978-824-97  
; Sequence 97, Application US/09978824  
; Publication No. US20030055216A1

## GENERAL INFORMATION:

;; APPLICANT: Ashkenazi, Avi  
;; APPLICANT: Baker Kevin P.  
;; APPLICANT: Botstein, David  
;; APPLICANT: Desnoyers, Luc  
;; APPLICANT: Eaton, Dan  
;; APPLICANT: Ferrara, Napoleon  
;; APPLICANT: Filvaroff, Ellen  
;; APPLICANT: Fong, Sherman  
;; APPLICANT: Gao, Wei-Qiang  
;; APPLICANT: Gerber, Hanspeter  
;; APPLICANT: Gerritsen, Mary E.  
;; APPLICANT: Goddard, Audrey  
;; APPLICANT: Godowski, Paul J.  
;; APPLICANT: Grimaldi, J. Christopher  
;; APPLICANT: Gurney, Austin L.  
;; APPLICANT: Hillan, Kenneth J.  
;; APPLICANT: Kljavit, Ivar J.  
;; APPLICANT: Kuo, Sophia S.  
;; APPLICANT: Napier, Mary A.  
;; APPLICANT: Pan, James  
;; APPLICANT: Paoni, Nicholas F.  
;; APPLICANT: Roy, Margaret Ann  
;; APPLICANT: Shelton, David L.  
;; APPLICANT: Stewart, Timothy A.  
;; APPLICANT: Tumas, Daniel  
;; APPLICANT: Williams, P. Mickey  
;; APPLICANT: Wood, William I.  
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
;; FILE REFERENCE: P2630P1C14  
;; CURRENT APPLICATION NUMBER: US/09/978,824  
;; CURRENT FILING DATE: 2001-10-17  
;; PRIOR APPLICATION NUMBER: 09/918585  
;; PRIOR FILING DATE: 2001-07-30  
;; PRIOR APPLICATION NUMBER: 60/062250

;; PRIOR FILING DATE: 1997-10-17  
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;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 153; DB 10; Length 277;  
Best Local Similarity 100.0%; Pred. No. 2e-16; 0;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CDCGRYKFKVGQLDISIALRLKTSMKFVKV 29  
Db 119 CDCGRYKFKVGQLDISIALRLKTSMKFVKV 147

## RESULT 15

US-09-918-585A-97  
; Sequence 97, Application US/09918585A  
; Publication No. US20030060406A1

## GENERAL INFORMATION:

;; APPLICANT: Ashkenazi, Avi  
;; APPLICANT: Baker Kevin P.  
;; APPLICANT: Botstein, David  
;; APPLICANT: Desnoyers, Luc  
;; APPLICANT: Eaton, Dan  
;; APPLICANT: Ferrara, Napoleon  
;; APPLICANT: Filvaroff, Ellen  
;; APPLICANT: Fong, Sherman  
;; APPLICANT: Gao, Wei-Qiang  
;; APPLICANT: Gerber, Hanspeter  
;; APPLICANT: Gerritsen, Mary E.  
;; APPLICANT: Goddard, Audrey  
;; APPLICANT: Godowski, Paul J.  
;; APPLICANT: Grimaldi, J. Christopher  
;; APPLICANT: Gurney, Austin L.  
;; APPLICANT: Hillan, Kenneth J.  
;; APPLICANT: Kljavin, Ivar J.  
;; APPLICANT: Kuo, Sophia S.  
;; APPLICANT: Napier, Mary A.  
;; APPLICANT: Pan, James;  
;; APPLICANT: Paoni, Nicholas F.  
;; APPLICANT: Roy, Margaret Ann  
;; APPLICANT: Shelton, David L.  
;; APPLICANT: Stewart, Timothy A.  
;; APPLICANT: Tumas, Daniel  
;; APPLICANT: Williams, P. Mickey  
;; APPLICANT: Wood, William I.  
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
;; TITLE OF INVENTION: Acids Encoding the Same  
;; FILE REFERENCE: P2630FICI  
;; CURRENT APPLICATION NUMBER: US/09/918,585A  
;; CURRENT FILING DATE: 2001-07-30  
;; PRIOR APPLICATION NUMBER: 60/062250  
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;; PRIOR FILING DATE: 1998-03-10

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Search completed: March 8, 2004, 12:18:57  
Job time : 11.4758 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 8, 2004, 12:07:46 ; Search time 7.53745 Seconds  
(without alignments)  
198.629 Million cell updates/sec

Title: US-09-600-932-2\_COPY\_119\_147

Perfect score: 153

Sequence: 1 CDCGRYKFGVQLDISIARLKTSMKFVN 29

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA.\*  
1: /cgn2\_6/ptodata/2/iaa/5A COMB.pep.\*  
2: /cgn2\_6/ptodata/2/iaa/5B COMB.pep.\*  
3: /cgn2\_6/ptodata/2/iaa/6A COMB.pep.\*  
4: /cgn2\_6/ptodata/2/iaa/6B COMB.pep.\*  
5: /cgn2\_6/ptodata/2/iaa/PTUS COMB.pep.\*  
6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	52	34.0	3635	4	US-09-845-583A-2
2	49	32.0	487	1	US-08-469-486-53
3	49	32.0	487	2	US-08-469-486-53
4	49	32.0	492	1	US-08-469-486-2
5	49	32.0	492	2	US-08-469-486-2
6	48	31.4	363	4	US-09-328-352-5961
7	47	30.7	113	4	US-09-134-001C-4973
8	46	30.1	106	4	US-09-107-532A-5116
9	46	30.1	279	3	US-09-318-794A-3
10	46	30.1	279	3	US-09-318-793A-5
11	46	30.1	459	3	US-09-118-319-6
12	46	30.1	459	3	US-09-286-691-2
13	46	30.1	459	3	US-09-687-147-2
14	45	29.4	37	6	5187155-10
15	45	29.4	50	6	5187155-9
16	45	29.4	238	4	US-09-664-595A-15
17	45	29.4	241	1	US-08-330-978-4
18	45	29.4	241	1	US-08-474-042-4
19	45	29.4	241	1	US-08-484-558-4
20	45	29.4	241	1	US-08-774-592-4
21	45	29.4	247	3	US-08-944-483-49
22	45	29.4	254	1	US-08-330-978-3
23	45	29.4	254	1	US-08-474-042-3
24	45	29.4	254	1	US-08-484-558-3
25	45	29.4	254	1	US-08-774-592-3
26	45	29.4	306	1	US-08-330-978-1
27	45	29.4	306	1	US-08-474-042-1

28 45 29.4 306 1 US-08-484-558-1 Sequence 1, Appli  
29 45 29.4 306 1 US-08-774-592-1 Sequence 1, Appli  
30 45 29.4 437 1 US-08-487-037-2 Sequence 2, Appli  
31 45 29.4 448 1 US-08-295-411-3 Sequence 3, Appli  
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33 45 29.4 448 5 PCT-US92-10068-1 Sequence 1, Appli  
34 45 29.4 448 5 PCT-US92-10242-3 Sequence 1, Appli  
35 45 29.4 488 1 US-08-487-037-1 Sequence 1, Appli  
36 45 29.4 488 4 US-09-367-777-44 Sequence 44, Appli  
37 45 29.4 488 4 US-09-367-791A-27 Sequence 27, Appli  
38 45 29.4 1024 4 US-09-562-737-83 Sequence 83, Appli  
39 44.5 29.1 393 3 US-08-977-554-2 Sequence 2, Appli  
40 44.5 29.1 393 3 US-09-225-967-2 Sequence 2, Appli  
41 44.5 29.1 393 3 US-09-227-806-2 Sequence 2, Appli  
42 44.5 29.1 758 4 US-08-735-101-2 Sequence 2, Appli  
43 44 28.8 573 4 US-09-134-001C-5026 Sequence 5026, Ap  
44 44 28.8 975 4 US-09-314-259-19 Sequence 19, Appli  
45 44 28.8 1024 4 US-09-562-737-84 Sequence 84, Appli

#### ALIGNMENTS

RESULT 1  
US-09-845-583A-2  
; Sequence 2, Application US/09845583A  
; Patent No. 6635616  
; GENERAL INFORMATION:  
; APPLICANT: Burgeson, Robert  
; APPLICANT: Brunken, William Joseph  
; APPLICANT: Champiaud, Marie-France  
; APPLICANT: Hunter, Dale  
; TITLE OF INVENTION: LAMININ 15 AND USES THEREOF  
; FILE REFERENCE: 10287-056001  
; CURRENT APPLICATION NUMBER: US/09/845,583A  
; CURRENT FILING DATE: 2001-04-30  
; PRIOR APPLICATION NUMBER: US 60/200,863  
; PRIOR FILING DATE: 2000-05-01  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 3635  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-845-583A-2

Query Match 34.0%; Score 52; DB 4; Length 3635;  
Best Local Similarity 43.5%; Pred. No. 55;  
Matches 10; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 4 GRYKFGVQLDISIARLKTSMKF 26  
DB 2636 GRVRKLIQAQSAASKVKVSMKF 2658

RESULT 2  
US-08-469-486-53  
; Sequence 53, Application US/08469486  
; Patent No. 5739281  
; GENERAL INFORMATION:  
; APPLICANT: Thoegeersen, Hans Christian  
; APPLICANT: Holtet, Thor Las  
; APPLICANT: Etzerodt, Michael  
; TITLE OF INVENTION: Improved method for the refolding of  
; NUMBER OF INVENTION: Proteins  
; NUMBER OF SEQUENCES: 58  
; CORRESPONDENCE ADDRESS:  
; ADDRESSES: Fish & Richardson  
; CITY: 225 Franklin Street  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02110-2804

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version  
SOFTWARE: #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/469,486  
FILING DATE:  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/192,060  
FILING DATE: February 4, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Paul T. Clark  
REGISTRATION NUMBER: 30,162  
REFERENCE/DOCKET NUMBER: 06363/002001  
TELEPHONE: 617 542 5070  
TELEFAX: 617 542 8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 53:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 487 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-469-486-53

Query Match 32.0%; Score 49; DB 1; Length 487;  
Best Local Similarity 40.0%; Pred. No. 18;  
Matches 10; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 5 RYKRVGQLDISIAKLTKSMKPVKN 29  
DB 312 RFVKETYDFDIAVLRLKTPIRFRN 336

RESULT 3  
US-08-469-658-53  
Sequence 53, Application US/08469658  
Patent No. 5917018  
GENERAL INFORMATION:  
APPLICANT: Th. egersen, Hans Christian  
APPLICANT: Holtet, Thor Las  
APPLICANT: Etzerodt, Michael  
TITLE OF INVENTION: IMPROVED METHOD FOR THE REFOLDING OF  
TITLE OF INVENTION: PROTEINS  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version  
SOFTWARE: #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/469,658  
FILING DATE: June 5, 1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/192,060  
FILING DATE: February 4, 1994  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Paul T. Clark

REGISTRATION NUMBER: 30,162  
REFERENCE/DOCKET NUMBER: 06363/002002  
TELEPHONE: 617 542 5070  
TELEFAX: 617 542 8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 53:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 487 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-469-658-53

Query Match 32.0%; Score 49; DB 2; Length 487;  
Best Local Similarity 40.0%; Pred. No. 18;  
Matches 10; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 5 RYKRVGQLDISIAKLTKSMKPVKN 29  
DB 312 RFVKETYDFDIAVLRLKTPIRFRN 336

RESULT 4  
US-08-469-486-2  
Sequence 2, Application US/08469486  
Patent No. 5739281  
GENERAL INFORMATION:  
APPLICANT: Thøgersen, Hans Christian  
APPLICANT: Holtet, Thor Las  
APPLICANT: Etzerodt, Michael  
TITLE OF INVENTION: Improved method for the refolding of  
TITLE OF INVENTION: proteins  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version  
SOFTWARE: #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/469,486  
FILING DATE:  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/192,060  
FILING DATE: February 4, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Paul T. Clark  
REGISTRATION NUMBER: 30,162  
REFERENCE/DOCKET NUMBER: 06363/002001  
TELEPHONE: 617 542 5070  
TELEFAX: 617 542 8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 492 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-469-486-2

Query Match 32.0%; Score 49; DB 1; Length 492;



[illegible]

APPLICATION NUMBER: US/09/107,532A  
FILING DATE: 30-Jun-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/085,598  
FILING DATE: 14 May 1998  
APPLICATION NUMBER: 60/051571  
FILING DATE: July 2, 1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Ariadello, Pamela Deneke  
REGISTRATION NUMBER: 40,489  
REFERENCE/DOCKET NUMBER: GTC-012  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (781) 893-5007  
TELEFAX: (781) 893-8277  
INFORMATION FOR SEQ ID NO: 5116:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 106 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: YES  
ORIGINAL SOURCE:  
ORGANISM: Enterococcus faecium  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (8) LOCATION 1...106  
SEQUENCE DESCRIPTION: SEQ ID NO: 5116:  
US-09-107-532A-5116

Query Match 30.1%; Score 46; DB 4; Length 106;  
Best Local Similarity 30.8%; Pred. No. 9.6;  
Matches 8; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

QY 4 GRYKRVQGLDISIARLK 29  
DB 70 GTIRKVSQYGLPVIKIDTIVRFKKS 95

RESULT 9  
US-09-318-794A-3  
Sequence 3, Application US/09318794A  
Patent No. 6177264  
GENERAL INFORMATION:  
APPLICANT: DEGUSSA AKTIENGESCHLAF  
TITLE OF INVENTION: METHOD FOR THE FERMENTATIVE PRODUCTION OF D-PANTOTHENIC  
TITLE OF INVENTION: ACID USING CORNEFORM BACTERIA  
FILE REFERENCE: eggeling  
CURRENT APPLICATION NUMBER: US/09/318,794A  
CURRENT FILING DATE: 1999-05-26  
PRIOR APPLICATION NUMBER: DE 198 55 312.9  
PRIOR FILING DATE: 1998-12-01  
NUMBER OF SEQ ID NOS: 9  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 3  
LENGTH: 279  
TYPE: PRT  
ORGANISM: Corynebacterium glutamicum  
US-09-318-794A-3

Query Match 30.1%; Score 46; DB 3; Length 279;  
Best Local Similarity 45.0%; Pred. No. 28;  
Matches 9; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 2 DCGYRKVFQGLDISIARLK 21  
DB 63 DCDYRNYPRQLDADLALLE 82

RESULT 10  
US-09-318-793A-5  
Sequence 5, Application US/09318793A  
Patent No. 6184007  
GENERAL INFORMATION:

APPLICANT: Dusch, Nicole  
APPLICANT: Kalinowski, Jorn  
APPLICANT: Puhler, Alfred  
TITLE OF INVENTION: METHOD FOR THE FERMENTATIVE PRODUCTION OF D-PANTOTHENIC  
TITLE OF INVENTION: ACID BY ENHANCEMENT OF THE pand GENE IN MICROORGANISMS  
FILE REFERENCE: 21123/260204  
CURRENT APPLICATION NUMBER: US/09/318,793A  
CURRENT FILING DATE: 1999-05-26  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 5  
LENGTH: 279  
TYPE: PRT  
ORGANISM: Corynebacterium glutamicum  
US-09-318-793A-5

Query Match 30.1%; Score 46; DB 3; Length 279;  
Best Local Similarity 45.0%; Pred. No. 28;  
Matches 9; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 2 DCGYRKVFQGLDISIARLK 21  
DB 63 DCDYRNYPRQLDADLALLE 82

RESULT 11  
US-09-118-319-6  
Sequence 6, Application US/09118319  
Patent No. 6114158  
GENERAL INFORMATION:  
APPLICANT: Li, Xin-liang  
APPLICANT: Chen, Huizhong  
APPLICANT: Ljungdahl, Lars G.  
TITLE OF INVENTION: Orpinomyces Cellulase Celf Protein and Coding Sequences  
FILE REFERENCE: 33-98sequence listing  
CURRENT APPLICATION NUMBER: US/09/118,319  
CURRENT FILING DATE: 1998-07-17  
NUMBER OF SEQ ID NOS: 9  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 6  
LENGTH: 459  
TYPE: PRT  
ORGANISM: Orpinomyces sp. PC-2  
US-09-118-319-6

Query Match 30.1%; Score 46; DB 3; Length 459;  
Best Local Similarity 50.0%; Pred. No. 48;  
Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 8 KFGVQGLDISIARLKTSMK 25  
DB 143 KFGVEVDISIKKLGDLK 160

RESULT 12  
US-09-286-691-2  
Sequence 2, Application US/09286691  
Patent No. 6190189  
GENERAL INFORMATION:  
APPLICANT: Li, Xin-Liang  
APPLICANT: Ljungdahl, Lars G.  
APPLICANT: Chen, Huizhong  
TITLE OF INVENTION: Cellulases and Coding Sequences  
FILE REFERENCE: 42-96  
CURRENT APPLICATION NUMBER: US/09/286,691  
CURRENT FILING DATE: 1999-04-05  
EARLIER APPLICATION NUMBER: US 60/027,883  
EARLIER FILING DATE: 1996-10-04  
EARLIER APPLICATION NUMBER: PCT US97/18008  
EARLIER FILING DATE: 1997-10-03  
NUMBER OF SEQ ID NOS: 29  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2

; LENGTH: 459  
; TYPE: PRT  
; ORGANISM: Oryzomyces sp. PC-2  
US-09-286-691-2

Query Match 30.1%; Score 46; DB 3; Length 459;  
Best Local Similarity 50.0%; Pred. No. 48;  
Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 8 KFGVGLDISIARLKTSMK 25  
|||:|||||:|  
Db 143 KFGGEVDISIKKNGDLK 160

RESULT 13

US-09-687-147-2  
; Sequence 2, Application US/09687147  
; Patent No. 6268198

; GENERAL INFORMATION:  
; APPLICANT: Li, Xin-Liang

; APPLICANT: Ljungdahl, Lars G.  
; APPLICANT: Chen, HuiZhong

; TITLE OF INVENTION: Cellulases and Coding Sequences  
; FILE REFERENCE: 42-96a

; CURRENT APPLICATION NUMBER: US/09/687,147  
; CURRENT FILING DATE: 2000-10-12

; PRIOR APPLICATION NUMBER: US 60/027,883  
; PRIOR FILING DATE: 1996-10-04

; PRIOR APPLICATION NUMBER: PCT US97/18008  
; PRIOR FILING DATE: 1997-10-03

; PRIOR APPLICATION NUMBER: 09/286,691  
; PRIOR FILING DATE: 1999-04-05

; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 2  
; LENGTH: 459

; TYPE: PRT  
; ORGANISM: Oryzomyces sp. PC-2

US-09-687-147-2

Query Match 30.1%; Score 46; DB 3; Length 459;  
Best Local Similarity 50.0%; Pred. No. 48;  
Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 8 KFGVGLDISIARLKTSMK 25  
|||:|||||:|  
Db 143 KFGGEVDISIKKNGDLK 160

RESULT 14

5187155-10

; Patent No. 5187155

; APPLICANT: FAIR, DARYL S.  
; TITLE OF INVENTION: ANTICOAGULANT PEPTIDES

; NUMBER OF SEQUENCES: 27  
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/371,561  
; FILING DATE: 23-JUN-1989

; SEQ ID NO:10:  
; LENGTH: 37

5187155-10

Query Match 29.4%; Score 45; DB 6; Length 37;  
Best Local Similarity 40.0%; Pred. No. 4.4;  
Matches 10; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

QY 5 RYRKFGVGLDISIARLKTSMKFKVN 29  
|||:|||||:|  
Db 7 RFTKETVDYDFDIIVLRLKPTIFRMN 31

RESULT 15

5187155-9

; Patent No. 5187155  
; APPLICANT: FAIR, DARYL S.  
; TITLE OF INVENTION: ANTICOAGULANT PEPTIDES  
; NUMBER OF SEQUENCES: 27  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/371,561  
; FILING DATE: 23-JUN-1989  
; SEQ ID NO:9:  
; LENGTH: 50

5187155-9

Query Match 29.4%; Score 45; DB 6; Length 50;  
Best Local Similarity 40.0%; Pred. No. 6;  
Matches 10; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

QY 5 RYRKFGVGLDISIARLKTSMKFKVN 29  
|||:|||||:|  
Db 20 RFTKETVDYDFDIIVLRLKPTIFRMN 44

Search completed: March 8, 2004, 12:17:28  
Job time : 8.53745 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 8, 2004, 11:54:00 ; Search time 26.7004 Seconds  
(without alignments)  
306.882 Million cell updates/sec

Title: US-09-600-932-2\_COPY\_119\_147

Perfect score: 153

Sequence: 1 CDCGRYKFKVQLDLSIARLKTSMKFKVN 29

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_29Jan04:\*

- 1: Geneseq1980s:\*
- 2: Geneseq1990s:\*
- 3: Geneseq2000s:\*
- 4: Geneseq2001s:\*
- 5: Geneseq2002s:\*
- 6: Geneseq2003as:\*
- 7: Geneseq2003bs:\*
- 8: Geneseq2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	153	100.0	159	5	ABB56404	Abb56404 Human col
2	153	100.0	277	2	AAY25518	Aay25518 Human col
3	153	100.0	277	2	AAY41698	Aay41698 Human PRO
4	153	100.0	277	3	AAB44254	Aab44254 Human PRO
5	153	100.0	277	4	AAU29073	Aau29073 Human PRO
6	153	100.0	277	6	ABU58449	Abu58449 Human PRO
7	153	100.0	277	6	ABU87997	Abu87997 Novel hum
8	153	100.0	277	6	ABU84312	Abu84312 Human sec
9	153	100.0	277	6	ABR66186	AbR66186 Human sec
10	153	100.0	277	6	ABR65576	AbR65576 Human sec
11	153	100.0	277	6	ABU99516	Abu99516 Human sec
12	153	100.0	277	6	ABU82755	Abu82755 Human PRO
13	153	100.0	277	6	ABU89876	Abu89876 Novel hum
14	153	100.0	277	6	ABR68125	AbR68125 Human sec
15	153	100.0	277	6	ABU96178	Abu96178 Novel hum
16	153	100.0	277	6	ABU92609	Abu92609 Human sec
17	153	100.0	277	6	ABO08686	AbO08686 Human sec
18	153	100.0	277	6	ABO02738	AbO02738 Human sec
19	153	100.0	277	6	ABR74892	AbR74892 Human sec
20	153	100.0	277	6	ABR94654	AbR94654 Human sec
21	153	100.0	277	6	ABO25200	AbO25200 Novel hum
22	153	100.0	277	6	ABU85627	Abu85627 Human PRO
23	153	100.0	277	6	ABU98787	Abu98787 Novel hum
24	153	100.0	277	6	ABU28002	Abu28002 Novel hum
25	153	100.0	277	6	ABU91708	Abu91708 Novel hum

Abu72206 Novel hum  
Abu89401 Human PRO  
Abu86242 Human sec  
Abu67455 Human sec  
Abu80483 Human PRO  
Abu99401 Human sec  
Abu98791 Human sec  
Abu16314 Human sec  
Abu92214 Human sec  
Abu18855 Human sec  
Abu78276 Human sec  
Abu85012 Novel hum  
Abu00151 Novel hum  
Abu011483 Human sec  
Abu021128 Human sec  
Abu88702 Novel hum  
Abu83397 Human sec  
Abu06198 Novel hum  
Abu59234 Human sec  
Abu09296 Human sec

## ALIGNMENTS

## RESULT 1

ABB56404  
ID ABB56404 standard; peptide; 159 AA.  
XX  
AC ABB56404;  
XX  
DT 19-FEB-2002 (first entry)  
XX  
DE Human collectin polypeptide SEQ ID NO 52.  
XX  
KW Human; collectin; CL-L2-1; CL-L2-2; mouse; antibacterial; virucide;  
KW protein therapy; infection; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO200181401-A1.  
XX  
PD 01-NOV-2001.  
XX  
PF 23-APR-2001; 2001WO-JF003468.  
XX  
PR 21-APR-2000; 2000JP-00120358.  
XX  
PA (FUSO ) FUSO PHARM IND LTD.  
XX  
PI Wakamiya N, Keshi H, Ohtani K, Sakamoto T, Kishi Y;  
XX  
DR WPI; 2002-055345/07.  
XX  
PT New collectin family proteins, designated CL-L2-1 and CL-L2-2, expressed  
PT in kidney and for treatment and prevention of bacterial and viral  
PT infections.  
XX  
PS Claim 8; Page 68; 134pp; Japanese.  
XX  
The invention relates to human collectin family proteins (CL-L2-1 and CL-L2-2, sequences given in the specification, ABB56407-ABB56411 and ABB56414-ABB56416), their derivatives and fragments and a related collectin (CL-L2) of mouse origin (ABB56412) and polynucleotides encoding all or part of the proteins. The proteins have antibacterial and virucide activity and are used for protein therapy and treatment, prevention and diagnosis of bacterial and viral infections. The present sequence is that of a collectin polynucleotide of the invention

SQ Sequence 159 AA;

Query Match 100.0%; Score 153; DB 5; Length 159;

Best Local Similarity 100.0%; Pred. No. 1.1e-15;

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Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CDCGRRKRVGQDLSIARLKTSMKFKVN 29
Db 1 CDCGRRKRVGQDLSIARLKTSMKFKVN 29

RESULT 2
AA41698
ID AAY25518 standard; protein; 277 AA.
AC AAY25518;
DT 30-SEP-1999 (first entry)
DE Human collectin protein.
KW Collectin; human; antibacterial; antiviral; treatment; infection.
OS Homo sapiens.
PN WO9937767-A1.
PD 29-JUL-1999.
PF 24-JUL-1998; 98WO-JP003328.
PR 23-JAN-1998; 98JP-00011281.
PX (FUSO ) FUSO PHARM IND LTD.
PA Wakamiya N;
PI PI
DR WPI; 1999-458691/38.
DX N-PSDB; AAX88323.
PT New collectin protein of human origin and DNA encoding it.
PS Claim 1; Page 42-44; 58pp; Japanese.
CC This invention describes the isolation and characterization of a novel
CC human collectin protein and its encoding polynucleotide. The human
CC collectin exhibits antibacterial and antiviral activity and can be used
CC as an agent for the treatment of human bacterial and viral infections.
CC This sequence represents the novel human collectin
SQ Sequence 277 AA;

Query Match 100.0%; Score 153; DB 2; Length 277;
Best Local Similarity 100.0%; Pred. No. 2e-15;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CDCGRRKRVGQDLSIARLKTSMKFKVN 29
Db 119 CDCGRRKRVGQDLSIARLKTSMKFKVN 147

RESULT 3
AA41698
ID AAY41698 standard; protein; 277 AA.
AC AAY41698;
DT 07-DEC-1999 (first entry)
DE Human PRO702 protein sequence.
KW Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;
KW probe; blood coagulation disorder; cancer; cellular adhesion disorder;
KW secreted protein; transmembrane protein.
OS Homo sapiens.
PN WO9946281-A2.
PD 16-SEP-1999.
PF 08-MAR-1999; 99WO-US005028.
PX 10-MAR-1998; 98US-0077450P.
PR 11-MAR-1998; 98US-0077632P.
PR 11-MAR-1998; 98US-0077641P.
PR 12-MAR-1998; 98US-0077791P.
PR 13-MAR-1998; 98US-0078004P.
PR 17-MAR-1998; 98US-00040220.
PR 20-MAR-1998; 98US-0078866P.
PR 20-MAR-1998; 98US-0078910P.
PR 20-MAR-1998; 98US-0078936P.
PR 25-MAR-1998; 98US-0078939P.
PR 26-MAR-1998; 98US-0079294P.
PR 27-MAR-1998; 98US-0079656P.
PR 27-MAR-1998; 98US-0079663P.
PR 27-MAR-1998; 98US-0079664P.
PR 27-MAR-1998; 98US-0079689P.
PR 27-MAR-1998; 98US-0079728P.
PR 27-MAR-1998; 98US-0079786P.
PR 30-MAR-1998; 98US-0079920P.
PR 30-MAR-1998; 98US-0079923P.
PR 31-MAR-1998; 98US-0080105P.
PR 31-MAR-1998; 98US-0080107P.
PR 31-MAR-1998; 98US-0080165P.
PR 31-MAR-1998; 98US-0080194P.
PR 01-APR-1998; 98US-0080327P.
PR 01-APR-1998; 98US-0080328P.
PR 01-APR-1998; 98US-0080333P.
PR 01-APR-1998; 98US-0080334P.
PR 08-APR-1998; 98US-0081049P.
PR 08-APR-1998; 98US-0081070P.
PR 08-APR-1998; 98US-0081071P.
PR 09-APR-1998; 98US-0081195P.
PR 09-APR-1998; 98US-0081203P.
PR 09-APR-1998; 98US-0081229P.
PR 15-APR-1998; 98US-0081817P.
PR 15-APR-1998; 98US-0081838P.
PR 15-APR-1998; 98US-0081952P.
PR 15-APR-1998; 98US-0081955P.
PR 21-APR-1998; 98US-0082568P.
PR 21-APR-1998; 98US-0082569P.
PR 22-APR-1998; 98US-0082700P.
PR 22-APR-1998; 98US-0082704P.
PR 22-APR-1998; 98US-0082804P.
PR 23-APR-1998; 98US-0082767P.
PR 23-APR-1998; 98US-0082796P.
PR 27-APR-1998; 98US-0083336P.
PR 28-APR-1998; 98US-0083322P.
PR 29-APR-1998; 98US-0083392P.
PR 29-APR-1998; 98US-0083495P.
PR 29-APR-1998; 98US-0083496P.
PR 29-APR-1998; 98US-0083499P.
PR 29-APR-1998; 98US-0083500P.
PR 29-APR-1998; 98US-0083545P.
PR 29-APR-1998; 98US-0083554P.
PR 29-APR-1998; 98US-0083558P.
PR 30-APR-1998; 98US-0083559P.
PR 30-APR-1998; 98US-0083742P.
PR 05-MAY-1998; 98US-0084366P.
PR 06-MAY-1998; 98US-0084414P.
PR 06-MAY-1998; 98US-0084415P.
PR 07-MAY-1998; 98US-0084598P.
PR 07-MAY-1998; 98US-0084600P.
PR 07-MAY-1998; 98US-0084627P.
PR 07-MAY-1998; 98US-0084637P.
PR 07-MAY-1998; 98US-0084639P.
PR 07-MAY-1998; 98US-0084640P.
PR 07-MAY-1998; 98US-0084643P.
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PR 13-MAY-1998; 98US-0085323P.  
PR 13-MAY-1998; 98US-0085338P.  
PR 13-MAY-1998; 98US-0085339P.  
PR 15-MAY-1998; 98US-0085573P.  
PR 15-MAY-1998; 98US-0085579P.  
PR 15-MAY-1998; 98US-0085580P.  
PR 15-MAY-1998; 98US-0085582P.  
PR 15-MAY-1998; 98US-0085689P.  
PR 15-MAY-1998; 98US-0085697P.  
PR 15-MAY-1998; 98US-0085700P.  
PR 18-MAY-1998; 98US-0085704P.  
PR 18-MAY-1998; 98US-0086023P.  
PR 22-MAY-1998; 98US-0086392P.  
PR 22-MAY-1998; 98US-0086414P.  
PR 22-MAY-1998; 98US-0086430P.  
PR 22-MAY-1998; 98US-0086486P.  
PR 28-MAY-1998; 98US-0087098P.  
PR 28-MAY-1998; 98US-0087106P.  
PR 28-MAY-1998; 98US-0087208P.  
PR 30-JUL-1998; 98US-0094651P.  
PR 11-SEP-1998; 98US-0100038P.  
XX (GETH ) GENENTECH INC.  
PA Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;  
PI WPI: 1999-551358/46.  
DR N-PSDB; AAZ333973.  
XX  
XX New secreted and transmembrane polypeptides and their polynucleotides,  
PT useful for treating blood coagulation disorders, cancers and cellular  
PT adhesion disorders.  
XX  
XX Claim 12; Fig 37; 530pp; English.  
PS  
XX The present invention describes secreted and transmembrane polypeptides  
CC and their polynucleotides. The nucleotide sequences are useful as sources  
CC of probes, primers, for chromosome mapping, and for generation of  
CC antisense sequences. They can also be used to create transgenic animals.  
CC The proteins can be used to treat a variety of diseases and disorders,  
CC depending on their function. Diseases that may be treated include blood  
CC coagulation disorders, cancers and cellular adhesion disorders. They may  
CC also be used to raise antibodies. AAZ33991 to AAZ4338, and AA41685 to  
CC AA41774 represent polynucleotide and polypeptide sequences given in the  
CC exemplification of the present invention  
XX  
XX Sequence 277 AA;  
SQ  
Query Match 100.0%; Score 153; DB 2; Length 277;  
Best Local Similarity 100.0%; Pred. No. 2e-15;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 CDCGRRKRVGQLDISIARLKTSMKFVK 29  
DB 119 CDCGRRKRVGQLDISIARLKTSMKFVK 147  
RESULT 4  
AAB44254  
ID AAB44254 standard; protein; 277 AA.  
XX AAB44254;  
XX AC  
XX AAB44254;  
DT 08-FEB-2001 (first entry)  
XX  
DE Human PRO702 (UNQ366) protein sequence SEQ ID NO:97.  
XX  
XX Human; secreted protein; transmembrane protein; PRO; EST; cytostatic;  
KW expressed sequence tag; detection; cancer.  
XX  
XX Homo sapiens.  
OS  
XX WO200053756-A2.  
PN

XX 14-SEP-2000.  
XX 18-FEB-2000; 2000WO-US004341.  
XX 08-MAR-1999; 99WO-US005028.  
PR 12-MAR-1999; 99US-0123957P.  
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PR 21-APR-1999; 99US-0130232P.  
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PR 14-MAY-1999; 99US-0134287P.  
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PR 26-JUL-1999; 99US-0145698P.  
PR 29-OCT-1999; 99US-0162506P.  
PR 30-NOV-1999; 99WO-US028313.  
PR 02-DEC-1999; 99WO-US028551.  
PR 16-DEC-1999; 99WO-US030095.  
PR 30-DEC-1999; 99WO-US031243.  
PR 30-DEC-1999; 99WO-US031274.  
PR 05-JAN-2000; 2000WO-US000219.  
PR 06-JAN-2000; 2000WO-US000277.  
PR 06-JAN-2000; 2000WO-US000376.  
XX (GETH ) GENENTECH INC.  
PA Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Baton DL;  
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;  
PI Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;  
PI Kljavin LJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;  
PI Stewart TA, Tumas D, Williams PM, Wood WI;  
XX WPI: 2000-611443/58.  
DR N-PSDB; AAC78480.  
XX  
XX Novel PRO polypeptides and polynucleotides used in detection methods, to  
PT target bioactive molecules to specific cells, and to modulate cellular  
PT activities.  
XX  
XX Claim 12; Fig 37; 636pp; English.  
XX  
XX AAC78458 to AAC78599 represent polynucleotide and EST (expressed sequence  
CC tag) sequences which encode secreted or transmembrane PRO polypeptides.  
CC The PRO polynucleotides and polypeptides have cytostatic activity. The  
CC polynucleotides and polypeptides can be used for detecting the presence  
CC of PRO polypeptides in samples, for linking bioactive molecules to cells  
CC and for modulating biological activities of cells, using the polypeptides  
CC and for specific targeting. The polypeptide targeting can be used to kill the  
CC target cells, e.g. for the treatment of cancers. The polypeptide pairs  
CC provide specific targeting of bioactive molecules to cells. AAC78600 to  
CC AAC78987 represent PCR primers and probes used in the isolation of the  
CC PRO polynucleotide sequences  
XX  
XX Sequence 277 AA;  
SQ  
Query Match 100.0%; Score 153; DB 3; Length 277;  
Best Local Similarity 100.0%; Pred. No. 2e-15;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 CDCGRRKRVGQLDISIARLKTSMKFVK 29  
DB 119 CDCGRRKRVGQLDISIARLKTSMKFVK 147  
RESULT 5  
AAU29073  
ID AAU29073 standard; protein; 277 AA.  
XX  
XX AC AAU29073;  
XX  
XX 18-DEC-2001 (first entry)  
XX  
XX Human PRO polypeptide sequence #50.  
DE

XX PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;  
KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;  
KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;  
KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.  
XX  
DS Homo sapiens.  
XX WO200168848-A2.  
XX  
XX 20-SEP-2001.  
XX  
XX 28-FEB-2001; 2001WO-US006520.  
XX  
XX 01-MAR-2000; 2000WO-US005601.  
XX 02-MAR-2000; 2000WO-US005841.  
XX 03-MAR-2000; 2000US-0187202P.  
XX 06-MAR-2000; 2000US-0186986P.  
XX 14-MAR-2000; 2000US-0189320P.  
XX 14-MAR-2000; 2000US-0189328P.  
XX 15-MAR-2000; 2000WO-US006884.  
XX 21-MAR-2000; 2000US-0190828P.  
XX 21-MAR-2000; 2000US-0191007P.  
XX 21-MAR-2000; 2000US-0191048P.  
XX 21-MAR-2000; 2000US-0191314P.  
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XX 29-MAR-2000; 2000US-0193032P.  
XX 29-MAR-2000; 2000US-0193053P.  
XX 30-MAR-2000; 2000WO-US008439.  
XX 04-APR-2000; 2000US-0194449P.  
XX 04-APR-2000; 2000US-0194647P.  
XX 11-APR-2000; 2000US-0195975P.  
XX 11-APR-2000; 2000US-0196000P.  
XX 11-APR-2000; 2000US-0196187P.  
XX 11-APR-2000; 2000US-0196690P.  
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XX 18-APR-2000; 2000US-0198121P.  
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XX 25-APR-2000; 2000US-0199397P.  
XX 25-APR-2000; 2000US-0199550P.  
XX 25-APR-2000; 2000US-0199654P.  
XX 03-MAY-2000; 2000US-0201516P.  
XX 17-MAY-2000; 2000WO-US013705.  
XX 22-MAY-2000; 2000WO-US014042.  
XX 30-MAY-2000; 2000WO-US014941.  
XX 02-JUN-2000; 2000WO-US015264.  
XX 05-JUN-2000; 2000US-0209832P.  
XX 28-JUL-2000; 2000WO-US020710.  
XX 22-AUG-2000; 2000US-00644848.  
XX 24-AUG-2000; 2000WO-US023328.  
XX 08-NOV-2000; 2000WO-US030952.  
XX 01-DEC-2000; 2000WO-US032678.  
XX 20-DEC-2000; 2000WO-US034956.  
XX  
XX (GETH ) GENENTECH INC.  
XX  
XX Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;  
XX Pan J, Smith V, Watanabe CK, Wood WJ, Zhang Z;  
XX  
XX WPI: 2001-602746/68.  
XX N-PSDB; AAS45974.  
XX  
XX Novel nucleic acids encoding PRO polypeptides, used to diagnose the  
XX presence of tumors, such as prostate and breast tumors, in mammals and to  
XX screen for modulators of the compounds.  
XX  
XX Claim 11; Fig 100; 774pp; English.  
XX  
XX Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.  
XX The PRO polypeptides and their associated nucleic acids can be used to  
XX detect the presence of a tumour in a mammal by comparing the level of  
XX expression of a PRO polypeptide in a test sample of cells from the animal  
XX and a control sample of normal cells, whereby a higher level of

CC expression in the test sample indicates the presence of a tumour in the  
CC mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats  
CC and rabbits but are preferably human. The polypeptides can be used to  
CC stimulate tumour necrosis factor (TNF) alpha release from human blood,  
CC when contacted with it. A specific polypeptide can be used to stimulate  
CC the proliferation or differentiation of chondrocyte cells. The PRO  
CC proteins can be used to determine the presence of tumours and also  
CC susceptibility to tumour development, particularly adrenal, lung, colon,  
CC breast, prostate, rectal, cervical, or liver tumours, in mammalian  
CC subjects. The oligonucleotide probes specific for the PRO nucleic acids  
CC can be used for genetic analysis of individuals with genetic disorders  
XX  
XX Sequence 277 AA;

Query Match 100.0%; Score 153; DB 4; Length 277;  
Best Local Similarity 100.0%; Pred. No. 2e-15;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDGGRYKFKVGLDTSIARLKTSMKFVKV 29  
Db 119 CDGGRYKFKVGLDTSIARLKTSMKFVKV 147

## RESULT 6

ABUS8449  
ID ABUS8449 standard; protein; 277 AA.

XX AC ABUS8449;

XX 15-APR-2003 (first entry)

XX DE Human PRO polypeptide #50.

XX KW Human; PRO; cytostatic; tumour; cancer; breast; lung; stomach; liver;  
XX dog; cat; cow; horse; sheep; pig; goat; rabbit; ADEPT;  
XX antibody-dependent enzyme mediated prodrug therapy.

XX OS Homo sapiens.

XX PN US2003027272-A1.

XX PD 06-FEB-2003.

XX 21-JUN-2002; 2002US-00176492.

XX 18-SEP-1997; 97US-0059263P.

XX 18-SEP-1997; 97US-0059266P.

XX 17-OCT-1997; 97US-0062250P.

XX 21-OCT-1997; 97US-0063486P.

XX 24-OCT-1997; 97US-0063120P.

XX 28-OCT-1997; 97US-0063121P.

XX 28-OCT-1997; 97US-0063540P.

XX 28-OCT-1997; 97US-0063541P.

XX 28-OCT-1997; 97US-0063544P.

XX 29-OCT-1997; 97US-0063734P.

XX 31-OCT-1997; 97US-0063870P.

XX 31-OCT-1997; 97US-0064103P.

XX 13-NOV-1997; 97US-0065311P.

XX 21-NOV-1997; 97US-0066120P.

XX 24-NOV-1997; 97US-0066466P.

XX 11-DEC-1997; 97US-0066772P.

XX 11-DEC-1997; 97US-0069335P.

XX 12-DEC-1997; 97US-0069425P.

XX 17-DEC-1997; 97US-0069870P.

XX 18-DEC-1997; 97US-0068017P.

XX 10-MAR-1998; 98US-0077450P.

XX 11-MAR-1998; 98US-0077632P.

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XX 20-MAR-1998; 98US-0078866P.

XX 20-MAR-1998; 98US-0078939P.

XX 27-MAR-1998; 98US-0079664P.

XX 27-MAR-1998; 98US-0079786P.

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PR 07-OCT-1998; 98US-00168978.

Query Match 100.0%; Score 153; DB 6; Length 277;
Best Local Similarity 100.0%; Pred. NO. 2e-15;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2y 1 CDCGRRKFKVQGLDISIARLKTSMKPVKN 29
db 119 CDCGRRKFKVQGLDISIARLKTSMKPVKN 147

RESULT 7
ABU87997
ID ABU87997 standard; protein; 277 AA.
XX
AC ABU87997;
XX
XX 07-JUL-2003 (first entry)
XX
XX Novel human secreted and transmembrane protein PRO702.
XX
XX Human; secreted and transmembrane protein; PRO: gene therapy;
XX tumour necrosis factor-alpha release; TNF-alpha release; tumour;
XX chondrocyte proliferation; chondrocyte differentiation; tumour;
XX adrenal tumour; lung tumour; colon tumour; breast tumour;
XX prostate tumour; rectal tumour; cervical tumour; liver tumour.
XX
XX Homo sapiens.
XX
XX US2003032127-A1.
XX
XX 13-FEB-2003.
XX
XX 26-JUN-2002; 2002US-00183012.
XX
PR 18-SEP-1997; 97US-0059263P.
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KW extracellular domain; tumour necrosis factor-alpha; TNF-alpha;  
KW chondrocyte; proliferation; differentiation; cartilage disorder;  
KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;  
KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;  
KW liver; drug screening; transgenic animal; genetic analysis;  
KW antiarthritic; vulnary; gene therapy.  
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OS Homo sapiens.  
XX  
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PD 06-FEB-2003.  
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ABR65576

ID ABR65576 standard; protein; 277 AA.

XX

AC ABR65576;

XX 05-AUG-2003 (first entry)  
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DE Human; PRO; secreted protein; transmembrane protein;  
XX extracellular domain; tumour necrosis factor-alpha; TNF-alpha;  
KW chondrocyte; proliferation; differentiation; cartilage disorder;  
KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;  
KW adrenal tumour; lung; colon; breast; prostate; kidney; cervix;  
KW liver; drug screening; transgenic animal; genetic analysis;  
KW antiarthritic; vulnery; gene therapy.  
XX Homo sapiens.  
OS  
XX US2003036159-A1.  
PN  
XX 20-FEB-2003.  
PD  
XX 02-JUL-2002; 2002US-00188773.  
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Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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ABU99516  
ID ABU99516 standard; protein; 277 AA.

XX AC ABU99516;

DT 09-AUG-2003 (first entry)

DE Human secreted/transmembrane protein (PRO) #50.

XX Human; secreted and transmembrane protein; PRO; TNF-alpha;  
KW tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;

KW tissue typing.  
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OS US2003040070-A1.  
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KX	Homo sapiens.				
2S	US2003032113-A1.				
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XX AC ABU89876;

XX 11-AUG-2003 (first entry)

XX DE Novel human secreted and transmembrane protein PRO702.

XX Human; gene therapy; tissue typing; tumour; chondrocyte proliferation;  
 KW chondrocyte differentiation; tumour necrosis factor-alpha release;  
 KW affinity purification.

XX OS Homo sapiens.

XX PN US2003036147-A1.

XX PD 20-FEB-2003.

XX PF 02-JUL-2002; 2002US-00187741.

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XX  
DT 11-AUG-2003 (first entry)  
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KW chondrocyte; proliferation; differentiation; cartilage disorder;  
KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;  
KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;  
KW liver; drug screening; transgenic animal; genetic analysis;  
KW antiarthritic; vulnary; Gene therapy.

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XX US2003027264-A1.  
XX  
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Best Local Similarity 100.0%; Pred. No. 2e-15;

Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 119 CDGGRYKFGQDISIARLKTSMKFVKN 147

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ID ABU96178 standard; protein; 277 AA.

XX AC ABU96178;

XX DT 25-JUL-2003 (first entry)

XX DE Novel human secreted and transmembrane protein PRO702.

XX KW Human; secreted and transmembrane protein; PRO; transgenic animal;  
knockout; chromosome identification; tissue typing; tumour;  
chondrocyte proliferation; chondrocyte differentiation;  
tumor necrosis factor-alpha release stimulator.

XX OS Homo sapiens.

XX US2003036144-A1.

XX PD 20-FEB-2003.

XX PF 01-JUL-2002; 2002US-00187601.

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Job time : 27.7004 secs

GenCore version 5.1.6  
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DM protein - protein search, using sw model

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Title: US-09-600-932-2\_COPY\_119\_147

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: Pir2.\*

3: Pir3.\*

4: Pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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1	144	94.1	277	2 JC7903	collectin liver 1
2	52	34.0	3635	2 T10053	laminin alpha 5 ch
3	49	32.0	188	2 140222	hypothetical prote
4	49	32.0	492	1 EXBO	coagulation factor
5	49	32.0	964	2 D59404	plectin isoform pl
6	49	32.0	1239	2 A45648	DNA topoisomerase
7	49	32.0	4574	2 G02520	plectin - human
8	49	32.0	4684	2 A59404	plectin (imported)
9	49	32.0	4687	1 A39638	plectin - rat
10	48	31.4	265	2 G96931	homocitrate syntha
11	48	31.4	465	2 A82211	Mut/mudix family
12	48	31.4	607	2 A95122	Tn5252 relaxase [
13	47.5	31.0	358	2 G96998	hypothetical prote
14	47	30.7	191	2 AH1571	alpha-ribazole-5'-
15	47	30.7	265	2 C90026	hypothetical prote
16	47	30.7	283	2 T50431	CBP3-like protein
17	46.5	30.4	581	2 P45599	probable kinesin h
18	46	30.1	279	2 T47120	pantoate-beta-alan
19	46	30.1	400	2 J24272	dcc2 protein - hum
20	46	30.1	447	2 A86647	hypothetical prote
21	46	30.1	491	2 T23527	hypothetical prote
22	46	30.1	508	2 A72201	UDP-sugar diphosph
23	46	30.1	604	2 S57065	probable membrane
24	45.5	29.7	167	2 P43114	methy coenzyme M
25	45.5	29.7	1295	2 T21720	hypothetical prote
26	45	28.4	127	2 AC1989	steroid delta-5-3-
27	45	29.4	279	2 G37246	araC-type DNA-bind
28	45	29.4	283	2 F95893	probable ABC trans
29	45	29.4	341	2 F90321	glycosyltransferas

hypothetical prote  
coagulation factor  
neoxanthin cleavag  
auxin-resistance p  
polyprotein - equi  
protein-glutamine  
hypothetical prote  
protein kinase hom  
DNA topoisomerase  
variant-specific s  
hypothetical prote  
protein F36A2.13 [   
connectin/titin -   
30S ribosomal prot  
coagulation factor  
probable membrane

ALIGNMENTS

RESULT 1

JC7903  
collectin liver 1 - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 03-Feb-2003 #sequence\_revision 03-Feb-2003 #text\_change 31-Mar-2003  
C:Accession: JC7903  
R:Kawai, T.; Suzuki, Y.; Eda, S.; Kase, T.; Ohtani, K.; Sakai, Y.; Keshi, H.; Fukuchi, A  
Biosci. Biotechnol. Biochem. 66, 2134-2145, 2002  
A:Title: Molecular cloning of mouse collectin liver 1.  
A:Reference number: JC7903; PMID:22333927; PMID:12450124  
A:Accession: JC7903  
A:Molecule type: mRNA  
A:Residues: 1-277 <RAW>  
A:Cross-references: DDBJ:AB016429  
A:Experimental source: liver  
C:Comment: This protein is a highly conserved cytosolic protein and belongs to a vertebr  
c development.  
C:Genetics:  
A:Gene: C111  
A:Map position: 15

Query Match 94.1%; Score 144; DB 2; Length 277;  
Best Local Similarity 89.7%; Pred. No. 2.5e-14;  
Matches 26; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Query 1 CDCGRRKFKVQGLDISIARLKTSMKFKVN 29

Db 119 CDCGRRKFKVQGLDISIARLKTSMKFKVN 147

RESULT 2

T10053  
laminin alpha 5 chain - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 21-Jul-2003  
C:Accession: T10053  
R:Miner, J.H.; Lewis, R.M.; Sanes, J.R.  
submitted to the EMBL Data Library, November 1997  
A:Reference number: Z16923  
A:Accession: T10053  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: mRNA  
A:Residues: 1-3635 <MIN>  
A:Cross-references: EMBL:U37501; NID:G2599231; PTD:G2599232  
C:Genetics:  
A:Gene: Lama5  
C:Keywords: basement membrane; cell binding; extracellular matrix  
F:1888-1939/Domain: laminin-type EGF-like homology <LEG>  
F:1942-1970/Domain: EGF homology <EGF>

Query Match 34.0%; Score 52; DB 2; Length 3635;  
Best Local Similarity 43.5%; Pred. No. 43;

Matches 10; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 4 GRYKRVGQLDISARLKTSMKF 26  
||| : : : |||  
Db 2636 GRVREKLIQAARSAASKVKVSMKF 2658

RESULT 3  
I40222  
Hypothetical protein 4 - Bacillus licheniformis (fragment)  
C:Species: Bacillus licheniformis  
C>Date: 12-Aug-1996 #sequence\_revision 12-Aug-1996 #text\_change 15-Oct-1999  
C:Accession: I40222  
R:Harry, E.J.; Partridge, S.R.; Weiss, A.S.; Wake, R.G.  
Gene 147, 85-89, 1994  
A>Title: Conservation of the 168 divIB gene in Bacillus subtilis W23 and B. licheniformis  
A:Reference number: I40220; MUID:94374713; PMID:8088553  
A:Accession: I40222  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-188 <REG>  
A:CROSS-references: EMBL:U01958; NID:9404008; PIDN:AAA57245.1; PID:G602399  
C:Genetics:  
A:Start codon: TTG

Query Match 32.0%; Score 49; DB 2; Length 188;  
Best Local Similarity 37.5%; Pred. No. 6.5;  
Matches 9; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 2 DCGRYKRVGQLDISARLKTSMK 25  
||| : : : |||  
Db 90 DVERYRMFVGIGVGEIGKIVTLK 113

RESULT 4  
EXPO  
coagulation factor Xa (EC 3.4.21.6) precursor - bovine  
N:Alternate names: Stuart factor  
C:Species: Bos primigenius taurus (cattle)  
C>Date: 24-Apr-1984 #sequence\_revision 17-Mar-1987 #text\_change 16-Jul-1999  
C:Accession: A22867; A14997; A12030; A34412; S39414; A00925  
R:Fung, M.R.; Campbell, R.M.; MacGillivray, T.A.  
Nucleic Acids Res. 12, 4481-4492, 1984  
A>Title: Blood coagulation factor X mRNA encodes a single polypeptide chain containing a  
A:Reference number: A22867; MUID:84247315; PMID:6330671  
A:Accession: A22867  
A:Molecule type: mRNA  
A:Residues: 1-487 <FUN>  
A:CROSS-references: GB:X00673; NID:G192; PIDN:CAA25286.1; PID:G193  
R:Enfield, D.L.; Ericsson, L.H.; Fujikawa, K.; Walsh, K.A.; Neurath, H.; Titani, K.  
Biochemistry 19, 659-667, 1980  
A>Title: Amino acid sequence of the light chain of bovine factor X-1 (Stuart factor).  
A:Reference number: A14997; MUID:80130563; PMID:6765735  
A:Accession: A14997  
A:Molecule type: protein  
A:Residues: 41-102, N', 104-180 <ENF>  
R:McMullen, B.A.; Fujikawa, K.; Kistiel, W.  
Biochem. Biophys. Res. Commun. 115, 8-14, 1983  
A>Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood co  
A:Reference number: A20274; MUID:83308813; PMID:6688526  
A:Contents: annotation; revision to residue 103  
R:Titani, K.; Fujikawa, K.; Enfield, D.L.; Ericsson, L.H.; Walsh, K.A.; Neurath, H.  
Proc. Natl. Acad. Sci. U.S.A. 72, 3082-3086, 1975  
A>Title: Bovine factor X-1 (Stuart factor): amino-acid sequence of heavy chain.  
A:Reference number: A12030; MUID:76053069; PMID:1059093  
A:Accession: A12030  
A:Molecule type: protein  
A:Residues: 183-292,294-295, GDE', 299-334, 336-349, 'AE', 351-354,356-441, 'GRKG', 446-492 <T  
A>Note: carboxylate binding sites and disulfide bonds were determined  
R:Ericsson, E.; Selander, M.; Linse, S.; Drakenberg, T.; Oellin, A.K.; Stenflo, J.  
J. Biol. Chem. 264, 16897-16904, 1989  
A>Title: Calcium binding to the isolated beta-hydroxyaspartic acid-containing epidermal  
A:Reference number: A34412; MUID:89380326; PMID:2789221

A:Accession: A34412  
A:Molecule type: protein  
A:Residues: 85-126 <PER>  
A>Note: beta-hydroxyaspartic acid site  
R:Inoue, K.; Morita, T.  
Eur. J. Biochem. 218, 153-163, 1993  
A>Title: Identification of O-linked oligosaccharide chains in the activation peptides of  
A:Reference number: S39414; MUID:94062825; PMID:8243461  
A:Accession: S39414  
A:Molecule type: protein  
A:Residues: 183-196,199-209;216-233 <INO>  
A>Note: carboxylate binding sites  
R:Titani, K.; Hermanson, M.A.; Fujikawa, K.; Ericsson, L.H.; Walsh, K.A.; Neurath, H.; I  
Biochemistry 11, 4899-4903, 1972  
A>Title: Bovine factor X-1a (activated Stuart factor). Evidence of homology with mammali  
A:Reference number: A12453; MUID:73053314; PMID:4264286  
A:Contents: annotation; active site  
R:Fujikawa, K.; Titani, K.; Davies, E.W.  
Proc. Natl. Acad. Sci. U.S.A. 72, 3359-3363, 1975  
A>Title: Activation of bovine factor X (Stuart factor): conversion of factor Xaalpha to  
A:Reference number: A13504; MUID:76053121; PMID:1059122  
A:Contents: annotation; activation  
R:Stigo, T.; Bjork, I.; Holmgren, A.; Stenflo, J.  
J. Biol. Chem. 259, 5705-5710, 1984  
A>Title: Calcium-binding properties of bovine factor X lacking the gamma-carboxyglutamic  
A:Reference number: A38024; MUID:84185716; PMID:6546930  
A:Contents: annotation; calcium binding  
R:Morita, T.; Jackson, C.M.  
J. Biol. Chem. 261, 4008-4014, 1986  
A:Reference number: A38025; MUID:86140210; PMID:3949800  
A:Contents: annotation; sulfate binding  
A:Comment: Factor Xa converts prothrombin to thrombin during blood clotting.  
C:Comment: The two chains are formed from a single-chain precursor by the excision of tv  
C:Comment: The activation peptide is cleaved by factor IXa (in the intrinsic pathway), c  
activation.  
C:Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with strc  
C:Comment: The gamma-carboxyglutamic acid residues arise by a posttranslational, vitamir  
C:Genetics:  
A:Gene: F10  
A:Map position: 13q34  
C:Function:  
A:Pathway: catalyzes the proteolytic activation of prothrombin to thrombin in the pr  
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology  
C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutan  
F:1-15/Domain: signal sequence #status predicted <SIG>  
F:16-40/Domain: propeptide #status predicted <PRO>  
F:45-84/Domain: Gla domain homology <GLA>  
F:129-164/Domain: EGF homology <EGF>  
F:183-233/Domain: coagulation factor X heavy chain #status experimental <HCH>  
F:234-492/Domain: coagulation factor Xa heavy chain #status experimental <AHC>  
F:234-461/Domain: trypsin homology <TRY>  
F:46,47,54,56,59,60,85,66,69,72,75,79/Modified site: gamma-carboxyglutamic acid (Glu) #s  
F:57-62,90-101,95-110,112-121,129-140,136-149,151-164,172-341/disulfide bonds: #status i  
F:103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental  
F:200/Binding site: sulfatate (Tyr) (covalent) (partial) #status experimental  
F:208,485/Binding site: carbohydurate (Thr) (covalent) #status experimental  
F:218/Binding site: carbohydurate (Asn) (covalent) #status experimental  
F:233-234/Cleavage site: Arg-11e [coagulation factor IXa, coagulation factor VIIa] #stat  
F:240-245,260-276,389-403,414-442/Disulfide bonds: #status experimental  
F:275,321,418/Active site: His, Asp, Ser #status predicted

Query Match 32.0%; Score 49; DB 1; Length 492;  
Best Local Similarity 40.0%; Pred. No. 17;  
Matches 10; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 5 RYRKEVGQLDISARLKTSMKFKVN 29  
||| : : : |||  
Db 312 RYRKEVGQLDISARLKTSMKFKVN 336



```
RESULT 5
D59404
Plectin isoform plectin 1.2alpha [imported] - mouse
C:Species: Mus musculus (house mouse)
C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C:Accession: D59404
R: Fuchs, P.; Zorer, M.; Reznicek, G.A.; Spazierer, D.; Oehler, S.; Castanon, M.J.; Hauptmann, M.; Genet, S.; 2461-2472, 1999
A: Title: Unusual 5' transcript complexity of plectin isoforms: novel tissue-specific exons
A: Reference number: D59404; MUID: 20025755; PMID: 10556294
A: Accession: D59404
A: Status: preliminary
A: Molecule type: DNA
A: Residues: 1-964 <STO>
A: Cross-references: GB:AAF18069; NID:G6578735; PIDN:AAF18069.1

Query Match 32.0%; Score 49; DB 2; Length 964;
Best Local Similarity 45.5%; Pred. No. 33;
Matches 10; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 4 GRYKFKVQGLDISIARLKTSMK 25
DB 733 GAYRDCGLRLDQYAKLLNSSK 754

RESULT 6
A45648
NA topoisomerase (ATP-hydrolyzing) (EC 5.99.1.3), kinetoplast-associated - Crithidia fasciculata
A: Alternate names: type II DNA topoisomerase
A: Species: Crithidia fasciculata
A: Date: 22-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
A: Accession: A45648; S15456
A: Pasion, S.G.; Hines, J.C.; Hebersold, R.; Ray, D.S.
A: Title: Molecular cloning and expression of the gene encoding the kinetoplast-associated type II DNA topoisomerase
A: Reference number: A45648; MUID: 92178291; PMID: 1311798
A: Accession: A45648
A: Molecule type: DNA; protein
A: Residues: 1-1239 <PAS>
A: Cross-references: EMBL:X59623; NID:G11000; PIDN:CAA42182.1; PID:G11001
A: Note: sequence extracted from NCBI backbone (NCBI:85204)
A: Comment: The same gene may encode the nuclear and kinetoplast (mitochondrial) forms of topoisomerase
A: Superfamily: eukaryotic type II DNA topoisomerase; phage T4 DNA topoisomerase (ATP-hydrolyzing); DNA binding; isomerase; mitochondrion; nucleus
A: Keywords: DNA binding; isomerase; mitochondrion; nucleus
A: Title: 891/DNA topoisomerase (ATP-hydrolyzing) medium chain homology <T4>

Query Match 32.0%; Score 49; DB 2; Length 1239;
Best Local Similarity 36.0%; Pred. No. 43;
Matches 9; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 5 RYKFKVQGLDISIARLKTSMKFVKV 29
DB 999 RRTQIGLLEMDLRLQSTKRFVEH 1023

RESULT 7
A02520
Plectin - human
C:Species: Homo sapiens (man)
C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 20-Aug-1999
C:Accession: G02520
A: McLean, W.H.T.; Smith, F.J.D.
A: Title: Submitted to the EMBL Data Library, March 1996
A: Reference number: H01385
A: Status: preliminary; translated from GB/EMBL/DBJ
A: Accession: G02520
A: Molecule type: mRNA
A: Residues: 1-4574 <MCL>
A: Cross-references: EMBL:U53204; NID:G1477645; PIDN:AB05427.1; PID:G1477646
A: Genetics:
A: Gene: PLEC1
A: Superfamily: plectin; alpha-actinin actin-binding domain homology; ribosomal protein S
```

F;68-283/Domain: alpha-actinin actin-binding domain homology <ACT>

```
Query Match 32.0%; Score 49; DB 2; Length 4574;
Best Local Similarity 45.5%; Pred. No. 1.6e+02;
Matches 10; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 4 GRYKFKVQGLDISIARLKTSMK 25
DB 615 GAYRDCGLRLDQYAKLLNSSK 636

RESULT 8
A59404
Plectin [imported] - human
C:Species: Homo sapiens (man)
C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 19-Apr-2002
C:Accession: C59404; A59404
R: Liu, C.G.; Maercker, C.; Castanon, M.J.; Hauptmann, R.; Wiche, G.
A: Title: Human plectin: organization of the gene, sequence analysis, and chromosome localization
A: Reference number: C59404; MUID: 96210632; PMID: 8633055
A: Accession: C59404
A: Status: preliminary
A: Molecule type: DNA
A: Residues: 1-4684 <STO>
A: Cross-references: GB:CAA91196; NID:G1296662; PIDN:CAA91196.1
A: Superfamily: plectin; alpha-actinin actin-binding domain homology; ribosomal protein S
```

```
Query Match 32.0%; Score 49; DB 2; Length 4684;
Best Local Similarity 45.5%; Pred. No. 1.6e+02;
Matches 10; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 4 GRYKFKVQGLDISIARLKTSMK 25
DB 725 GAYRDCGLRLDQYAKLLNSSK 746
```

```
RESULT 9
A39638
Plectin - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C:Accession: A39638; S21876
R: Wiche, G.; Becker, B.; Lubber, K.; Weitzer, G.; Castanon, M.J.; Hauptmann, R.; Stratowa, J.
A: Title: Cloning and sequencing of rat plectin indicates a 466-kD polypeptide chain with a 466-kD polypeptide chain with
A: Reference number: A39638; MUID: 91268156; PMID: 2050743
A: Accession: A39638
A: Status: preliminary
A: Molecule type: mRNA
A: Residues: 1-4687 <WIC>
A: Cross-references: EMBL:X59601; NID:G1292885; PIDN:CAA42169.1; PID:G1561642
A: Superfamily: plectin; alpha-actinin actin-binding domain homology; ribosomal protein S
A: Keywords: cytoskeleton; transmembrane protein
A: Title: 103/DNA topoisomerase (ATP-hydrolyzing) medium chain homology <RS10>
A: Title: 399/DNA topoisomerase (ATP-hydrolyzing) medium chain homology <ACT>

Query Match 32.0%; Score 49; DB 1; Length 4687;
Best Local Similarity 45.5%; Pred. No. 1.6e+02;
Matches 10; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 4 GRYKFKVQGLDISIARLKTSMK 25
DB 728 GAYRDCGLRLDQYAKLLNSSK 749
```

```
RESULT 10
G96931
homocitrate synthase, alpha chain nifv(nioh) [imported] - Clostridium acetobutylicum
C:Species: Clostridium acetobutylicum
C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
A: Accession: G96931
A: Noll, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
```

; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.  
J. Bacteriol. 183, 4823-4838, 2001  
A>Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo  
A;Reference number: A96900; MUID:21359325; PMID:21359325  
A;Accession: G96931  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-265 <KUR>  
A;Cross-references: GB:AE001437; PIDN:AAK78242.1; PID:gl5023098; GSPDB:GN00168  
A;Experimental source: Clostridium acetobutylicum ATCC824  
A;Gene: CAC0261

Query Match 31.4%; Score 48; DB 2; Length 265;  
Best Local Similarity 31.0%; Pred. No. 13;  
Matches 9; Conservative 7; Mismatches 13; Indels 0; Gaps 0;

QY 1 CDGGRYKRVGQLDISIALKTSKMFVK 29  
DB 229 CDGGRYKRVGQLDISIALKTSKMFVK 29

RESULT 11  
A82211  
MUTX/nudix family protein VC1342 [imported] - Vibrio cholerae (strain N16961 serogroup C  
C;Species: Vibrio cholerae  
C;Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 02-Feb-2001  
C;Accession: A82211  
R;Heidelberger, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;  
chardson, D.; Ermlaeva, M.D.; Yamathavan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, E  
l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.  
Nature 406, 477-483, 2000  
A>Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.  
A;Reference number: A82035; MUID:20406833; PMID:10952301  
A;Accession: A82211  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-465 <HEI>  
A;Cross-references: GB:AE004214; GB:AE003852; NID:g9655832; PIDN:AAF94500.1; GSPDB:GN001  
A;Experimental source: serogroup O1; strain N16961; biotype El Tor  
C;Genetics:  
A;Gene: VC1342  
A;Map position: 1

Query Match 31.4%; Score 48; DB 2; Length 465;  
Best Local Similarity 40.9%; Pred. No. 23;  
Matches 9; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 8 KFGVGLDISIALKTSKMFVK 29  
DB 175 EWLGLQHGVAQKKSMPLQN 196

RESULT 12  
A95122  
Tns252, relaxase [imported] - Streptococcus pneumoniae (strain TIGR4)  
C;Species: Streptococcus pneumoniae  
C;Date: 03-Aug-2001 #sequence\_revision 03-Aug-2001 #text\_change 03-Aug-2001  
C;Accession: A95122  
R;Hettlin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid  
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple,  
nson, T.; Hickey, E.K.; Holt, I.E.  
Science 293, 498-506, 2001  
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,  
A>Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.  
A;Reference number: A95000; MUID:21357209; PMID:11463916  
A;Accession: A95122  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-607 <KUR>  
A;Cross-references: GB:AE005672; PIDN:AAK75170.1; PID:gl4972530; GSPDB:GN00164; TIGR:SP4  
A;Experimental source: strain TIGR4  
C;Genetics:

A;Gene: SP1056

Query Match 31.4%; Score 48; DB 2; Length 607;  
Best Local Similarity 52.4%; Pred. No. 30;  
Matches 11; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 4 GRYEKRVGQLDISIALKTSK 24  
DB 577 GRYEKRVGQLDISIALKTSK 597

RESULT 13  
G96998  
Hypothetical protein CAC0802 [imported] - Clostridium acetobutylicum  
C;Species: Clostridium acetobutylicum  
C;Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 14-Sep-2001  
C;Accession: G96998  
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,  
; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.  
J. Bacteriol. 183, 4823-4838, 2001  
A>Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo  
A;Reference number: A96900; MUID:21359325; PMID:21359325  
A;Accession: G96998  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-358 <KUR>  
A;Cross-references: GB:AE001437; PIDN:AAK78778.1; PID:gl5023690; GSPDB:GN00168  
A;Experimental source: Clostridium acetobutylicum ATCC824  
C;Genetics:  
A;Gene: CAC0802

Query Match 31.0%; Score 47.5; DB 2; Length 358;  
Best Local Similarity 42.9%; Pred. No. 21;  
Matches 12; Conservative 3; Mismatches 12; Indels 1; Gaps 1;

QY 1 CDCGRYKRVGQLDISIALKTSKMFVK 28  
DB 104 CKRGYKRIIGPVDAF-WLKRYMKINK 130

RESULT 14  
AH1571  
alpha-ribazole-5'-phosphatase homolog lin113 [imported] - Listeria innocua (strain Clif  
C;Species: Listeria innocua  
C;Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 03-Nov-2003  
C;Accession: AH1571  
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bicecker  
; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, E.  
D.; Jones, L.M.; Karat, U.  
Science 294, 849-852, 2001  
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma  
ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,  
A>Title: Comparative genomics of Listeria species  
A;Reference number: AB1077; MUID:21537279; PMID:11679669  
A;Accession: AH1571  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-191 <GLA>  
A;Cross-references: GB:AL592022; PIDN:CAC96344.1; PID:gl6413572; GSPDB:GN00178  
A;Experimental source: strain Clif11262  
C;Genetics:  
A;Gene: lin113  
C;Superfamily: cofactor-dependent phosphoglycerate mutase; phosphoglycerate mutase homol

Query Match 30.7%; Score 47; DB 2; Length 191;  
Best Local Similarity 37.5%; Pred. No. 13;  
Matches 6; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 2 DCGRYKRVGQLDISI 17  
DB 12 DCNALKKYGQMDVAL 27



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 8, 2004, 12:02:31 ; Search time 61.3216 Seconds  
(without alignments)  
411.624 Million cell updates/sec

Title: US-09-600-932-2\_COPY\_148\_227

Perfect score: 417

Sequence: 1 VIAGIRETEKFFYIVQEEK.....FIGVNDLEREGQVMFTDTP 80

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:\*

1: sp\_archaea:\*

2: sp\_bacteria:\*

3: sp\_fungi:\*

4: sp\_human:\*

5: sp\_invertebrate:\*

6: sp\_mammal:\*

7: sp\_mhc:\*

8: sp\_organelle:\*

9: sp\_phase:\*

10: sp\_plant:\*

11: sp\_rodent:\*

12: sp\_virus:\*

13: sp\_vertebrate:\*

14: sp\_unclassified:\*

15: sp\_rvirus:\*

16: sp\_bacteriap:\*

17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	DB ID	Description
1	417	100.0	277	4	Q9Y6Z7 homo sapien
2	405	97.1	277	11	Q8CF98
3	405	97.1	277	11	Q8CLC5
4	255	61.2	271	13	Q7T0T0
5	254	60.9	272	11	Q9DC75
6	250	60.0	268	4	Q7Z6N1
7	250	60.0	271	4	Q9BWP8
8	113.5	27.2	251	13	Q919Q8
9	106	25.4	238	13	Q57451
10	106	25.4	254	13	Q987R4
11	105	25.2	201	13	Q9DD44
12	103.5	24.8	1292	5	Q9DD44 Gallus gall
13	97	23.3	381	5	Q8WSW7
14	96	23.0	145	5	Q8WSW6
15	96	23.0	263	5	Q8WTP3
16	96	23.0	263	5	Q24696

17	93.5	22.4	222	13	Q90XB2
18	93.5	22.4	399	6	Q8HY12
19	93	22.3	246	13	Q919Q7
20	93	22.3	256	13	Q919Q9
21	90.5	21.7	404	6	Q8HY00
22	90.5	21.7	404	6	Q8HXZ9
23	90	21.6	208	11	Q91ZW7
24	89.5	21.5	399	6	Q8HY10
25	89	21.3	236	13	Q8UUM9
26	89	21.3	262	5	Q8WTP2
27	89	21.3	381	5	Q8WSW8
28	88.5	21.2	268	4	Q96QQ3
29	88.5	21.2	312	4	Q96Q07
30	88.5	21.2	334	4	Q96QF9
31	88.5	21.2	360	4	Q96Q04
32	88.5	21.2	380	4	Q96Q05
33	88.5	21.2	380	4	Q96Q00
34	88.5	21.2	404	4	Q96Q01
35	88.5	21.2	404	4	Q9NNX6
36	88.5	21.2	427	6	Q8HYB9
37	88	21.1	196	11	Q9EPM4
38	88	21.1	652	5	Q8WSX0
39	88	21.1	826	5	Q9VPS3
40	87.5	21.0	404	6	Q9SL98
41	87.5	21.0	422	6	Q8HY11
42	87.5	21.0	427	6	Q8HXZ7
43	87	20.9	163	13	Q8AXR8
44	86.5	20.7	312	6	Q8HXL6
45	86.5	20.7	381	6	Q95LC6

ALIGNMENTS

RESULT 1

Q9Y6Z7	PRELIMINARY;	PRT;	277 AA.
AC	Q9Y6Z7;		
DT	01-NOV-1999 (TREMBLrel. 12, Created)		
DT	01-NOV-1999 (TREMBLrel. 12, Last sequence update)		
DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)		
DE	Collectin 34.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
RN	[1]		
RX	NCBI_taxid=9606;		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=99240768; PubMed=10224141;		
RA	Ohtani K., Suzuki Y., Eda S., Kawai T., Kase T., Yamazaki H.,		
RA	Keishi H., Sakai Y., Fukuhara A., Sakamoto T., Wakamiya N.,		
RT	"Molecular cloning of a novel collectin from liver (CL-L1).";		
RL	J. Biol. Chem. 274:13681-13689(1999).		
DR	EMBL; AB002631; BAA81747.1; -		
DR	HSP; P19999; 2MSB.		
DR	Genew; HGNC:2220; COLEC10.		
DR	GO; GO:0005737; C:cytoplasm; TAS.		
DR	GO; GO:0005530; F:lectin; TAS.		
DR	InterPro; IPR008160; Collagen.		
DR	InterPro; IPR001304; LECTIN_C.		
DR	Pfam; PF01391; Collagen; 1.		
DR	Pfam; PF00059; lectin c; 1.		
DR	SMART; SM00034; CLECT; 1.		
DR	PROSITE; PS00615; C TYPE LECTIN 1; 1.		
DR	PROSITE; PS00041; C TYPE LECTIN 2; 1.		
SQ	SEQUENCE 277 AA; 30733 MW; 9736861CEBDC5C25 CRC64;		

Query Match 100.0%; Score 417; DB 4; Length 277;

Best Local Similarity 100.0%; Pred. No. 7.2e-41;

Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VIAGIRETEKFFYIVQEEKYRESLTHCRIRGGMLAMPKDEANTLIADYVAKSGFRV 60

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Db 148 VIAGIRETEKFFYIVQBEKNYRESLTHCRIRGGLAMPKDEAANTLIADYVAKSGFFRV 207
QY 61 FIGVNDLEREGQYFTDNT 80
Db 208 FIGVNDLEREGQYFTDNT 227

RESULT 2
Q8CF98 PRELIMINARY; PRT; 277 AA.
AC Q8CF98;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Collectin-L1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RX MEDLINE=22333927; PubMed=12450124;
RA Kawai T., Suzuki Y., Eda S., Kase T., Ohtani K., Sakai Y., Keshi H.,
RA Fukuoh A., Sakamoto T., Nozaki M., Copeland N.G., Jenkins N.A.,
RA Wakamiya N.;
RT "Molecular Cloning of Mouse Collectin Liver 1.";
RL Biosci. Biotechnol. Biochem. 66:2134-2145 (2002).
DR EMBL; AB016429; BACS3954.1; -.
DR GO; GO:0005529; P:sugar binding; IEA.
DR InterPro; IPR008160; Collagen.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF01391; Collagen; 1.
DR Pfam; PF00059; lectin c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR PROSITE; PS00041; C_TYPE_LECTIN_2; 1.
DR PROSITE; PS00041; C_TYPE_LECTIN_2; 1.
SQ SEQUENCE 277 AA; 30524 MW; 98C743A2E07A2872 CRC64;

Query Match 97.1%; Score 405; DB 11; Length 277;
Best Local Similarity 96.2%; Pred. No. 1.9e-39;
Matches 77; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 VIAGIRETEKFFYIVQBEKNYRESLTHCRIRGGLAMPKDEAANTLIADYVAKSGFFRV 60
Db 148 VIAGIRETEKFFYIVQBEKNYRESLTHCRIRGGLAMPKDEAANTLIADYVAKSGFFRV 207
QY 61 FIGVNDLEREGQYFTDNT 80
Db 208 FIGVNDLEREGQYFTDNT 227

RESULT 3
Q8C1C5 PRELIMINARY; PRT; 277 AA.
AC Q8C1C5;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Collectin-34 homolog.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA The RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
```

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DR EMBL; AK028423; BAC25941.1; -.
DR GO; GO:0005529; P:sugar binding; IEA.
DR InterPro; IPR008160; Collagen.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF01391; Collagen; 1.
DR Pfam; PF00059; lectin c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR PROSITE; PS00041; C_TYPE_LECTIN_2; 1.
SQ SEQUENCE 277 AA; 30510 MW; 94EF23A2E5404872 CRC64;

Query Match 97.1%; Score 405; DB 11; Length 277;
Best Local Similarity 96.2%; Pred. No. 1.9e-39;
Matches 77; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 VIAGIRETEKFFYIVQBEKNYRESLTHCRIRGGLAMPKDEAANTLIADYVAKSGFFRV 60
Db 148 VIAGIRETEKFFYIVQBEKNYRESLTHCRIRGGLAMPKDEAANTLIADYVAKSGFFRV 207
QY 61 FIGVNDLEREGQYFTDNT 80
Db 208 FIGVNDLEREGQYFTDNT 227

RESULT 4
Q7T0T0 PRELIMINARY; PRT; 271 AA.
AC Q7T0T0;
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Hypothetical protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22341132; PubMed=12454917;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
```

RA Klein S., Strausberg R.;  
RL Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC056052; AAH56052.1; -  
KW Hypothetical protein.  
SQ SEQUENCE 271 AA; 29334 MW; 587129273C476AE2 CRC64;

Query Match 61.2%; Score 255; DB 13; Length 271;  
Best Local Similarity 56.2%; Pred. No. 9.2e-22;  
Matches 45; Conservative 18; Mismatches 17; Indels 0; Gaps 0;

QY 1 VIAGIRETEEFYIVQBEKNYRESLTHCRIRGGLAMPKDEAANTLIADYVAKSGFFRVF 60  
Db 142 VVAGVRETETKIYLLVKEKKYDAQDYCQCGGGTSLMPKDEAINTLIASVYHAGLSRV 201  
QY 61 FIGVNDLREGGYMTDNTP 80  
Db 202 FIGINDLEREGHYVSDRSP 221

RESULT 5  
Q9DC75 PRELIMINARY; PRT; 272 AA.  
AC Q9DC75  
DT 01-JUN-2001 (TRENBLrel. 17, Created)  
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)  
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)  
DE 1010001H16RIK.  
GN 1010001H16RIK.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Heart;  
RX MEDLINE=21085660; PubMed=11217851;  
RA Kawai J., Hinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,  
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
RA Kadota K., Matsuda H.A., Abburner M., Batalov S., Casavant T.,  
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
RA Kuehl P., Lewis S., Matsuo Y., Nkaido I., Pesole G., Quackenbush J.,  
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
RA Gustincich S., Hall D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,  
RA Wyszaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,  
RA Hayashizaki Y.;  
RT Functional annotation of a full-length mouse cDNA collection.;  
RL Nature 409:685-690(2001).  
DR EMBL; AK03121; BAB2581.1; -  
DR HSSP; P22897; IEQG.  
DR MGD; MGI:1918943; 1010001H16RIK.  
DR GO; GO:0005529; F:sugar binding; IEA.  
DR InterPro; IPR008160; Collagen.  
DR InterPro; IPR001304; Lectin.C.  
DR Pfam; PF01391; Collagen; 1.  
DR Pfam; PF00059; lectin c; 1.  
DR SMART; SM00034; CLECT; 1.  
DR PROSITE; PS00615; C-TYPE LECTIN 1; 1.  
DR PROSITE; PS50041; C-TYPE LECTIN 2; 1.  
SQ SEQUENCE 272 AA; 28975 MW; DEC471493CD16B95 CRC64;

Query Match 60.9%; Score 254; DB 11; Length 272;  
Best Local Similarity 55.7%; Pred. No. 1.2e-21;  
Matches 44; Conservative 19; Mismatches 16; Indels 0; Gaps 0;

QY 2 IAGIRETEEFYIVQBEKNYRESLTHCRIRGGLAMPKDEAANTLIADYVAKSGFFRVF 61  
Db 144 VAGVRETESKIYLLVKEKKYDAQQLSCQARGGTSLMPKDEAANGLMASYLAQAGLARVF 203  
QY 62 IGVDLREREGGYMTDNTP 80  
Db 204 IGINDLEKEGAFVYSDRSP 222

RESULT 6  
Q7Z6N1 PRELIMINARY; PRT; 268 AA.  
AC Q7Z6N1  
DT 01-OCT-2003 (TRENBLrel. 25, Created)  
DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)  
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)  
DE MGC3279 protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Tothiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Boak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villard D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnarch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RA Strausberg R.;  
RL Submitted (Jul-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC009951; AAH09951.1; -  
SQ SEQUENCE 268 AA; 29005 MW; 30C30CC8258AA9B7 CRC64;

Query Match 60.0%; Score 250; DB 4; Length 268;  
Best Local Similarity 55.7%; Pred. No. 3.6e-21;  
Matches 44; Conservative 20; Mismatches 15; Indels 0; Gaps 0;

QY 2 IAGIRETEEFYIVQBEKNYRESLTHCRIRGGLAMPKDEAANTLIADYVAKSGFFRVF 61  
Db 140 VAGVRETESKIYLLVKEKKYDAQQLSCQARGGTSLMPKDEAANGLMASYLAQAGLARVF 199  
QY 62 IGVDLREREGGYMTDNTP 80  
Db 200 IGINDLEKEGAFVYSDRSP 218

RESULT 7  
Q9BWP8 PRELIMINARY; PRT; 271 AA.  
AC Q9BWP8  
DT 01-JUN-2001 (TRENBLrel. 17, Created)  
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)  
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)

DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RA Strussberg R.;  
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC000078; AAH00078.1; -.  
DR HSSP; P22897; 1EG3.  
DR GO; GO:0005529; F:sugar binding; IEA.  
DR InterPro; IPR008160; Collagen.  
DR InterPro; IPR001304; Lectin\_C.  
DR Pfam; PF01391; Collagen; 1.  
DR Pfam; PF00059; lectin\_c; 1.  
DR SMART; SM00034; CLECT; 1.  
DR PROSITE; PS00615; C\_TYPE\_LLECTIN\_1; 1.  
DR PROSITE; PS00041; C\_TYPE\_LLECTIN\_2; 1.  
KW Hypothetical protein.  
SQ SEQUENCE 271 AA; 28665 MW; A14A248CE41DB340 CRC64;  
  
Query Match 60.0%; Score 250; DB 4; Length 271;  
Best Local Similarity 55.7%; Pred. No. 3.6e-21;  
Matches 44; Conservative 20; Mismatches 15; Indels 0; Gaps 0;  
  
QY 2 IAGIRETEKFFYIVQEEKNYRESLTHCRIRGGMAMPKDEAANTLIADYVAKSGFFRVF 61  
143 VAGVRETSKIYLLVKEKRYADQLSQRGGLTSPKDEANGLMAYLAQAGLARVF 202  
62 IGVNDLEREGQVMTDNTP 80  
203 IGINDLEKGAFFVSDHSP 221  
  
RESULT 8  
Q91908 PRELIMINARY; PRT; 251 AA.  
AC Q91908;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Mannose binding-like lectin precursor.  
GN MBL  
OS Brachydanio rerio (Zebrafish) (Danio rerio).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Danio.  
OX NCBI\_TaxID=7955;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20456722; PubMed=11003389;  
RA Vitved L., Holmskov U., Koch C., Teisner B., Hansen S., Skjold K.;  
RT "The homologue of mannose-binding lectin in the carp family Cyprinidae  
is expressed at high level in spleen, and the deduced primary  
structure predicts affinity for galactose.";  
RL Immunogenetics 51:955-964(2000).  
DR EMBL; AF227738; BA63469.1; -.  
DR HSSP; P19959; IAFB.  
DR ZFIN; ZDB-GENE-000427-2; mbl.  
DR GO; GO:0005529; F:sugar binding; IEA.  
DR GO; GO:0007157; P:heterophilic cell adhesion; IEA.  
DR InterPro; IPR008161; Clg helix.  
DR InterPro; IPR008160; Collagen.  
DR InterPro; IPR001304; Lectin\_C.  
DR Pfam; PF01391; Collagen; 2.  
DR Pfam; PF00059; lectin\_c; 1.  
DR ProDom; PD000007; Clg\_helix; 1.  
DR SMART; SM00034; CLECT; 1.  
DR PROSITE; PS00615; C\_TYPE\_LLECTIN\_1; 1.  
DR PROSITE; PS00041; C\_TYPE\_LLECTIN\_2; 1.  
KW Collagen; Lectin; Signal.

FT SIGNAL 1 23 POTENTIAL.  
FT CHAIN 24 251 MANNOSE BINDING-LIKE LECTIN.  
FT VARIANT 21 M -> L.  
FT VARIANT 204 K -> N.  
SQ SEQUENCE 251 AA; 26829 MW; 12D0ABD06B6E3B11 CRC64;  
  
Query Match 27.2%; Score 113.5; DB 13; Length 251;  
Best Local Similarity 30.6%; Pred. No. 4.2e-05;  
Matches 22; Conservative 20; Mismatches 29; Indels 1; Gaps 1;  
  
QY 6 RETEBKFFYIVQEEKNYRESLTHCRIRGGMAMPKDEAANTLIADYVAKSGFFRVFIGN 65  
131 KVGQKYVTVDDVEETFDKGMQYCSSNGGALVLPRTLEENALLKVFVS-SAFKRLFIRIT 189  
66 DLREEGQVMTD 77  
190 DREKGEFVDTD 201  
  
RESULT 9  
O57451 PRELIMINARY; PRT; 238 AA.  
ID O57451;  
AC O57451 (TrEMBLrel. 06, Created)  
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)  
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Mannan-binding lectin (Fragment).  
GN CMBL  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=White Leghorn; TISSUE=Liver;  
RA Laursen S.B.;  
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF022226; AAB94071.1; -.  
DR HSSP; P19999; LYTT.  
DR GO; GO:0005529; F:sugar binding; IEA.  
DR GO; GO:0007157; P:heterophilic cell adhesion; IEA.  
DR InterPro; IPR008161; Clg helix.  
DR InterPro; IPR008160; Collagen.  
DR InterPro; IPR001304; Lectin\_C.  
DR Pfam; PF01391; Collagen; 1.  
DR Pfam; PF00059; lectin\_c; 1.  
DR ProDom; PD000007; Clg\_helix; 1.  
DR SMART; SM00034; CLECT; 1.  
DR PROSITE; PS00615; C\_TYPE\_LLECTIN\_1; 1.  
DR PROSITE; PS00041; C\_TYPE\_LLECTIN\_2; 1.  
KW Collagen; Lectin.  
FT NON\_TER 238  
SQ SEQUENCE 238 AA; 25645 MW; E5C9B5197AAE64E3 CRC64;  
  
Query Match 25.4%; Score 106; DB 13; Length 238;  
Best Local Similarity 28.2%; Pred. No. 0.00031;  
Matches 20; Conservative 20; Mismatches 29; Indels 2; Gaps 1;  
  
QY 10 EKFFYIVQEEKNYRESLTHCRIRGGMAMPKDEAANTLIADYVAKSGFFRVFIGNDLER 69  
126 KMFVSTGKYNFEKSKLCAKAGSVLAFRNEAENTALKDLIDFSS--QAYIGISDAQT 183  
70 EGQVMTDNTP 80  
184 EGFRWYLSGGP 194  
  
RESULT 10  
Q98TA4 PRELIMINARY; PRT; 254 AA.  
ID Q98TA4;  
AC Q98TA4;  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)

DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Mannose-binding lectin protein precursor.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20456722; PubMed=11003389;  
 RA Vitved L., Holmskov U., Koch C., Teisner B., Hansen S., Skjoldt K.;  
 RT "The homologue of mannose-binding lectin in the carp family Cyprinidae  
 is expressed at high level in spleen, and the deduced primary  
 structure predicts affinity for galactose."  
 RL Immunogenetics 51:955-964(2000).  
 DR EMBL; AF231714; AAK30298.1; --  
 DR HSSP; P19999; 1YTT  
 DR GO; GO:0005622; C:intracellular; IEA.  
 DR GO; GO:0005529; F:sugar binding; IEA.  
 DR GO; GO:0003700; F:transcription factor activity; IEA.  
 DR GO; GO:0007157; P:heterophilic cell adhesion; IEA.  
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
 DR InterPro; IPR008161; Clg helix.  
 DR InterPro; IPR000005; HTHArac.  
 DR InterPro; IPR001304; Lectin\_C.  
 DR Pfam; PF01391; Collagen; 1.  
 DR Pfam; PF00059; lectin\_C; 1.  
 DR ProDom; PD000007; Clg helix; 1.  
 DR SMART; SM00034; CLECT; 1.  
 DR PROSITE; PS00615; C\_TYPE\_LLECTIN\_1; 1.  
 DR PROSITE; PS00041; C\_TYPE\_LLECTIN\_2; 1.  
 DR PROSITE; PS00041; HTH\_ARAC\_FAMILY\_1; 1.  
 KW Collagen; Lectin; Signal.  
 FT SIGNAL 1 21  
 FT CHAIN 22 254  
 FT VARIANT 234 234 D -> V.  
 FT SEQUENCE 254 AA; 27376 MW; C924428643441AED CRC64;  
 Query Match 25.4%; Score 106; DB 13; Length 254;  
 Best Local Similarity 28.2%; Pred. No. 0.00033;  
 Matches 20; Conservative 20; Mismatches 29; Indels 2; Gaps 1;  
 2Y 10 EKFYVIOEKNYRESLTHCRIGGLAMPKRAANTLIADYVAKSFFRVFTGYNDLER 69  
 DB 142 KMFVSTGKKNFKGLKAGSVLSPRNEANTALKDLIDPS--QAVIGISDAQT 199  
 2Y 70 EGQYMTDNT 80  
 DB 200 EGRFWYLSGGP 210  
 RESULT 11  
 29DDDD4  
 ID Q9DDD4 PRELIMINARY; PRT; 201 AA.  
 AC Q9DDD4;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Tetraactin.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX Wever U.M.;  
 RT "tetraactin in chicken."  
 RL Submitted (Mar-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ271116; CAC20217.1; --  
 DR HSSP; P05452; 1TN3.

DR GO; GO:0005529; F:sugar binding; IEA.  
 DR InterPro; IPR001304; Lectin\_C.  
 DR InterPro; IPR003990; Pancrreatis\_ac.  
 DR Pfam; PF00059; lectin\_C; 1.  
 DR PRINTS; PR01504; PNCREATISAP.  
 DR SMART; SM00034; CLECT; 1.  
 DR PROSITE; PS00615; C\_TYPE\_LLECTIN\_1; 1.  
 DR PROSITE; PS00041; C\_TYPE\_LLECTIN\_2; 1.  
 DR PROSITE; PS00041; C\_TYPE\_LLECTIN\_2; 1.  
 SQ SEQUENCE 201 AA; 22172 MW; 7C7F235D24426AE8 CRC64;  
 Query Match 25.2%; Score 105; DB 13; Length 201;  
 Best Local Similarity 30.6%; Pred. No. 0.00033;  
 Matches 22; Conservative 15; Mismatches 33; Indels 2; Gaps 1;  
 11 KFYVIOEKNYRESLTHCRIGGLAMPKRAANTLIADYVAKS--GFFRVFTGYNDLE 68  
 DB 79 KCFLAPSEKTYHEASEHCISQGTGTTGQGBENDALDYMKSIGNEAEIWLGLNDWV 138  
 QY 69 REGQYMTDNT 80  
 DB 139 AEGKWVDMTGSP 150  
 RESULT 12  
 Q9VQ68  
 ID Q9VQ68 PRELIMINARY; PRT; 1292 AA.  
 AC Q9VQ68;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE CG15378 protein.  
 GN LECTIN-22C OR CG15378.  
 OS Drosophila melanogaster. (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Berkley;  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celnikier S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.P.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G.,  
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Frankoch C., Baldwin D.,  
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,  
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Fabois B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Flesler C., Gabrielian A.B., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
 RA Jaitani M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Kusekern D.R., Pacleb J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reiner K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupek M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,



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RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
DR EMBL; AB003584; AAF51313.1; -.
DR HSSP; P05452; 1TN3.
DR FlyBase; FBgn040105; lectin-22C.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008061; P:chitin binding; IEA.
DR GO; GO:0005529; F:sugar binding; IEA.
DR GO; GO:0006030; P:chitin metabolism; IEA.
DR InterPro; IPR002557; Chitin bind_Pera.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF01607; CBM 14; 3.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00494; CLEBD2; 3.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS50041; C-TYPE LECTIN 2; 1.
SQ SEQUENCE 1292 AA; 142942 MW; 327C0F3968B2BBC8 CRC64;

Query Match 24.8%; Score 103.5; DB 5; Length 1292;
Best Local Similarity 34.7%; Pred. No. 0.0043;
Matches 25; Conservative 15; Mismatches 29; Indels 3; Gaps 2;

QY 4 GIRETEEFYIVQ-EEKNYRESLTHCRIRGMLAMPKDEAANTLIADYVAKSGFFRVFI 62
Db 138 GFEQIGSKYVYIEKYSEKNWSTASKCNMGHLADIKDEADLAIAKANLKEDTHV--WL 195
QY 63 GYNDLEREQYM 74
Db 196 GINDLDHEGKFL 207

RESULT 13
Q8WSW7 PRELIMINARY; PRT; 381 AA.
AC Q8WSW7;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Scarf3b.
GN SCARF3B.
OS Dugesia tigrina (Planarian).
OC Eukaryota; Metazoa; Platyhelminthes; Turbellaria; Seriata; Tricladida;
OC Paludicola; Dugesidae; Girardia.
OX NCBI_TaxID=6162;
RN [1]
RP SEQUENCE FROM N.A.
RA Bogdanova E.A., Shagin D., Lukyanov K.A., Barsova E.V., Punkova N.,
RA Usman N., Matz M., Gurskaya N., Lukyanov S.A.;
RT "Characterization of a novel family of C-type lectin proteins from
planaria entitled multi-domain free lectins.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY057977; AAL29935.1; -.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 3.
DR SMART; SM00034; CLECT; 3.
DR PROSITE; PS00615; C-TYPE LECTIN 1; 3.
DR PROSITE; PS50041; C-TYPE LECTIN 2; 3.
SQ SEQUENCE 381 AA; 43996 MW; F34922A2B17FA87F CRC64;

Query Match 23.3%; Score 97; DB 5; Length 381;
Best Local Similarity 23.3%; Pred. No. 0.0061;
Matches 17; Conservative 22; Mismatches 34; Indels 0; Gaps 0;

QY 8 TEKFPYIVQSEKNYRESLTHCRIRGMLAMPKDEAANTLIADYVAKSGFFRVFIGVNDL 67
Db 17 TQACYHLNKNKNYNDVAVKYCNSEKRLVKITDSQTNAAVFELASKNGMGTYWNGNDI 76
QY 68 EREGQYMTDNTP 80
Db 68 EREGQYMTDNTP 80

RESULT 14
Q8WSW6 PRELIMINARY; PRT; 145 AA.
AC Q8WSW6;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Scarf1.
GN SCARF1.
OS Dugesia tigrina (Planarian).
OC Eukaryota; Metazoa; Platyhelminthes; Turbellaria; Seriata; Tricladida;
OC Paludicola; Dugesidae; Girardia.
OX NCBI_TaxID=6162;
RN [1]
RP SEQUENCE FROM N.A.
RA Bogdanova E.A., Shagin D., Lukyanov K.A., Barsova E.V., Punkova N.,
RA Usman N., Matz M., Gurskaya N., Lukyanov S.A.;
RT "Characterization of a novel family of C-type lectin proteins from
planaria entitled multi-domain free lectins.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY057980; AAL29937.1; -.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C-TYPE LECTIN 1; 1.
DR PROSITE; PS50041; C-TYPE LECTIN 2; 1.
SQ SEQUENCE 145 AA; 16670 MW; 3D1337BBE477CB25 CRC64;

Query Match 23.0%; Score 96; DB 5; Length 145;
Best Local Similarity 23.3%; Pred. No. 0.0026;
Matches 17; Conservative 22; Mismatches 34; Indels 0; Gaps 0;

QY 8 TEKFPYIVQSEKNYRESLTHCRIRGMLAMPKDEAANTLIADYVAKSGFFRVFIGVNDL 67
Db 17 TQACYHLNKNKNYNDVAVKYCNSEKRLVKITDSQTNAAVFELASKNGMGTYWNGNDI 76
QY 68 EREGQYMTDNTP 80
Db 68 EREGQYMTDNTP 80

RESULT 15
Q8WTF3 PRELIMINARY; PRT; 263 AA.
AC Q8WTF3;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Scarf2.
GN SCARF2.
OS Dugesia tigrina (Planarian).
OC Eukaryota; Metazoa; Platyhelminthes; Turbellaria; Seriata; Tricladida;
OC Paludicola; Dugesidae; Girardia.
OX NCBI_TaxID=6162;
RN [1]
RP SEQUENCE FROM N.A.
RA Bogdanova E.A., Matz M., Tarabykin V., Usman N., Shagin D., Zaraisky A.,
RA Lukyanov S.;
RT "Inductive interactions regulating body patterning in planarian,
revealed by analysis of expression of novel gene scarf.";
RL Dev. Biol. 194:172-181(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Bogdanova E.A., Shagin D., Lukyanov K.A., Barsova E.V., Punkova N.,
RA Usman N., Matz M., Gurskaya N., Lukyanov S.A.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY057975; AAL29933.1; -.
DR 68 EREGQYMTDNTP 80
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Db 77 AIEGTWVDTENKP 89
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77 AIEGTWVDTENKP 89

RESULT 14
Q8WSW6 PRELIMINARY; PRT; 145 AA.
AC Q8WSW6;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Scarf1.
GN SCARF1.
OS Dugesia tigrina (Planarian).
OC Eukaryota; Metazoa; Platyhelminthes; Turbellaria; Seriata; Tricladida;
OC Paludicola; Dugesidae; Girardia.
OX NCBI_TaxID=6162;
RN [1]
RP SEQUENCE FROM N.A.
RA Bogdanova E.A., Shagin D., Lukyanov K.A., Barsova E.V., Punkova N.,
RA Usman N., Matz M., Gurskaya N., Lukyanov S.A.;
RT "Characterization of a novel family of C-type lectin proteins from
planaria entitled multi-domain free lectins.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY057980; AAL29937.1; -.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C-TYPE LECTIN 1; 1.
DR PROSITE; PS50041; C-TYPE LECTIN 2; 1.
SQ SEQUENCE 145 AA; 16670 MW; 3D1337BBE477CB25 CRC64;

Query Match 23.0%; Score 96; DB 5; Length 145;
Best Local Similarity 23.3%; Pred. No. 0.0026;
Matches 17; Conservative 22; Mismatches 34; Indels 0; Gaps 0;

QY 8 TEKFPYIVQSEKNYRESLTHCRIRGMLAMPKDEAANTLIADYVAKSGFFRVFIGVNDL 67
Db 17 TQACYHLNKNKNYNDVAVKYCNSEKRLVKITDSQTNAAVFELASKNGMGTYWNGNDI 76
QY 68 EREGQYMTDNTP 80
Db 68 EREGQYMTDNTP 80

RESULT 15
Q8WTF3 PRELIMINARY; PRT; 263 AA.
AC Q8WTF3;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Scarf2.
GN SCARF2.
OS Dugesia tigrina (Planarian).
OC Eukaryota; Metazoa; Platyhelminthes; Turbellaria; Seriata; Tricladida;
OC Paludicola; Dugesidae; Girardia.
OX NCBI_TaxID=6162;
RN [1]
RP SEQUENCE FROM N.A.
RA Bogdanova E.A., Matz M., Tarabykin V., Usman N., Shagin D., Zaraisky A.,
RA Lukyanov S.;
RT "Inductive interactions regulating body patterning in planarian,
revealed by analysis of expression of novel gene scarf.";
RL Dev. Biol. 194:172-181(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Bogdanova E.A., Shagin D., Lukyanov K.A., Barsova E.V., Punkova N.,
RA Usman N., Matz M., Gurskaya N., Lukyanov S.A.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY057975; AAL29933.1; -.
DR 68 EREGQYMTDNTP 80
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DR EMBL; AY057974; AAL29933.1; JOINED.
DR GO; GO:0005529; F.sugar binding; IEA.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 2.
DR SMART; SM00034; CLECT; 2.
DR PROSITE; PS00615; C-TYPE LECTIN 1; 2.
DR PROSITE; PS00041; C-TYPE LECTIN 2; 2.
SQ SEQUENCE 263 AA; 30301 MW; 07D62BEEBBD1266B CRC64;

Query Match      23.0%; Score 96; DB 5; Length 263;
Best Local Similarity 23.3%; Pred.No. 0.0052;
Matches 17; Conservative 22; Mismatches 34; Indels 0; Gaps 0;

QY 8 TEEKFYIVQEEKYRESLTHCRIRGGMAMPKDEAANTLIADYVAKSGPFRVFIGVNDL 67
Db 17 TQAYVHLNKNKNVNDVAVKYNCKEIRLVKITDSQTNAAVVELASKNGMGTYWNGNDI 76
QY 68 EREGQYMTDNTTP 80
Db 77 AIEGTWVDTENKP 89
```

Search completed: March 8, 2004, 12:15:14  
Job time : 62.3216 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 8, 2004, 11:56:05 ; Search time 12.6872 Seconds  
(without alignments)  
328.331 Million cell updates

```

Title:      US-09-600-932-2_COPY_148_227
Perfect score: 417
Sequence:   1 VIAGRIETEKFYIVQEEK.....FIGVNDIEREGVMFTDNTP 80

```

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

Post-processing:	Minimum Match	0%
	Maximum Match	100%
	Listing first	45 s

Database : SwissProt 42:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Query			ID	Description
	Score	Match	Length		
1	91	21.8	166	1	TETN CARSP
2	85	20.4	197	1	CLEF_HUMAN
3	83.5	20.0	369	1	PSPD_BOVIN
4	82	19.7	202	1	TETN_HUMAN
5	81.5	19.5	321	1	CL43_BOVIN
6	81.5	19.5	371	1	CL46_BOVIN
7	81.5	19.5	1456	1	MANR_HUMAN
8	79.5	19.1	374	1	PSPD_MOUSE
9	78.5	18.8	248	1	PSFA_HUMAN
10	78	18.7	202	1	TETN_MOUSE
11	78	18.7	328	1	SCGF_MOUSE
12	78	18.7	328	1	SCGF_RAT
13	77.5	18.6	550	1	KUCR_RAT
14	76.5	18.3	371	1	CONG_BOVIN
15	76.5	18.3	548	1	KUCR_MOUSE
16	74	17.7	238	1	MABA_RAT
17	73.5	17.6	155	1	PLC_HALLA
18	73	17.3	1722	1	LY75_HUMAN
19	72	17.3	323	1	SCGF_HUMAN
20	71.5	17.1	374	1	PSPD_RAT
21	71.5	17.1	1450	1	SRRJ_STRPU
22	70.5	16.9	331	1	FCR2_MOUSE
23	70.5	16.9	1458	1	PAKR_RABIT
24	69.5	16.7	162	1	LECG_MEGRO
25	69.5	16.7	1463	1	PAJR_BOVIN
26	69	16.5	828	1	MRXC_KLEPN
27	67.5	16.2	247	1	PSPA_CAVPO
28	66.5	15.9	375	1	PSPD_HUMAN
29	66.5	15.9	872	1	TE95_TETTH
30	66	15.8	249	1	MABC_BOVIN
31	65.5	15.7	628	1	FTSH_PORPU
32	64.5	15.5	207	1	LECH_CHICK
33	64	15.3	746	1	TDCE_SCOLI

34	63.5	15.2	314	1	YDGH_ECOLI	P76177	escherichia
35	63	15.1	239	1	MABA_MOUSE	P39039	mus musculus
36	63	15.1	912	1	PCGB_BOVIN	Q28062	bos taurus
37	63	15.1	1723	1	LW75_MOUSE	Q60767	mus musculus
38	62.5	15.0	118	1	VATF_YEAST	P39111	saccharomyc
39	62.5	15.0	248	1	PSPA_CANFA	P06908	canis famil
40	62.5	15.0	388	1	TEPB_EUCAI	Q45685	buchnera ap
41	62.5	15.0	878	1	VAVZ_HUMAN	P52735	homo sapien
42	62	14.9	271	1	FPG_HAEIN	P49548	haemophilus
43	62	14.9	571	1	HBMN_NDVIJ	P35742	newcastle d
44	62	14.9	582	1	PGMU_PEA	Q9sm60	pisum sativ
45	62	14.9	604	1	HPV1_HPV36	P59808	human papil

## ALIGNMENTS

```

RESULT 1
ID      TETN_CARSP      STANDARD;      PRT;      166 AA.
AC      P26258;
DT      01-MAY-1992 (Rel. 22, Created)
DT      01-MAY-1992 (Rel. 22, Last sequence update)
DT      15-MAR-2004 (Rel. 43, Last annotation update)
DE      Tetranectin-like protein.
OS      Carcharias springeri (Reef shark).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC      Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;
OC      Carcharhinidae; Carcharhinus.
NCBI_TaxID=7809;
RN      [1];
RP      SEQUENCE.
RC      TISSUE=Neural arch cartilage;
RX      MEDLINE=93284081; PubMed=1304877;
RA      Neame P.J., Young C.N., Treep J.T.;
RT      "Primary structure of a protein isolated from reef shark
RT      (Carcharhinus springeri) cartilage that is similar to the mammalian
RT      C-type lectin homolog, tetranectin.";
RL      Protein Sci. 1:161-168(1992).
CC      1- SIMILARITY: Contains 1 C-type lectin family domain.
DR      PIR; A37289; A37289.
DR      HSSP; P05452; 1HTN.
DR      InterPro; IPR001304; Lectin C.
DR      SMART; PF00059; lectin_C; 1.
DR      SMART; SMO0034; CLECT; 1.
DR      PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR      PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
DR      KX      Lectin.
DR      FT      DOMAIN      43      161      C-TYPE LECTIN.
FT      DISULFID      37      47
FT      DISULFID      64      160
FT      DISULFID      136      152
SQ      SEQUENCE      166 AA; 18432 MW; 53EF812DEA5C6119 CRC64;

Query Match      21.8%; Score 91; DB 1; Length 166;
Best Local Similarity      28.8%; Pred. No. 0.0027;
Matches      21; Conservative      15; Mismatches      35; Indels      2; Gaps      1;

QY      10 EKFFVIVQEEKYRESLTHCRIGGGMLAMPKDEAANTLIADYVAKS--GFFRVFVGVNDL 67
DB      45 KCVLIASRGSKSYHAANEDCIAAGTILSPRSDEGNSLSRYAKSLVGARDFWIGNDM 104
      ||:::|
      105 TTEGKFVDVNGLP 117

QY      68 EREGQYMFDTNTP 80
DB      105 TTEGKFVDVNGLP 117

RESULT 2
CLEL_HUMAN
ID      CLEL_HUMAN      STANDARD;      PRT;      197 AA.
AC      O75596;
DT      28-FEB-2003 (Rel. 41, Created)
DT      28-FEB-2003 (Rel. 41, Last sequence update)

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10-OCT-2003 (Rel. 42, Last annotation update)
C-type lectin superfamily member 1 precursor (Cartilage-derived C-type
lectin).
CLCSCF1.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
TISSUE=Cartilage;
MEDLINE=99453719; PubMed=10524194;
Neame P.J., Tapp H., Grimm D.R.;
"The cartilage-derived, C-type lectin (CLCSCF1): structure of the gene
and chromosomal location.";
Biochim. Biophys. Acta 1446:193-202(1999).
-!- TISSUE SPECIFICITY: Restricted to cartilage.
-!- SIMILARITY: Contains 1 C-type lectin family domain.
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EMBL; AF077345; AAD12542.1; -.
EMBL; AF077344; AAD12542.1; JOINED.
HSSP; P05452; IHTN.
Genew; HGNC:2052; CLCSCF1.
GO; GO:0005530; F:lectin; TAS.
GO; GO:0001501; P:skeletal development; TAS.
InterPro; IPR001304; Lectin_C.
Pfam; PF00059; lectin_c; 1.
SMART; SM00034; CLECT; 1.
PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
PROSITE; PS00041; C_TYPE_LECTIN_2; 1.
Lectin; Signal.
CHAIN 1 22 POTENTIAL.
C-YPE LECTIN SUPERFAMILY MEMBER 1.
DOMAIN 23 197 C-YPE LECTIN.
C-YPE LECTIN.
DISULFID 68 78 BY SIMILARITY.
DISULFID 95 191 BY SIMILARITY.
DISULFID 167 183 BY SIMILARITY.
SEQUENCE 197 AA; 22232 MW; BB924DBDB7729A4 CRC64;
Query Match 20.4%; Score 85; DB 1; Length 197;
Best Local Similarity 25.7%; Pred. No. 0.016;
Matches 18; Conservative 20; Mismatches 30; Indels 2; Gaps 1;
2Y 7 ETEKFFYIVQEEKNYRESLTHCRIRGGLAMPKDEAAANTLIADYVAKS--GFPRVFIGV 64
3B 73 KVHKCYLASGLGHFHEANEDCISKGLIVIPRNSDEINALQDYGRSLPGVDFWLGI 132
2Y 65 NDLREGQYIM 74
3B 133 NDVMEGKVF 142
RESULT 3
2SPD_BOVIN
ID_PSPD_BOVIN STANDARD; PRT; 369 AA.
AC_P35246;
JT 01-FEB-1994 (Rel. 28, Created)
JT 01-FEB-1994 (Rel. 28, Last sequence update)
JT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Pulmonary surfactant-associated protein D precursor (SP-D) (PSP-D).
3N SFTPD OR SFTPA.
3S Bos taurus (Bovine).
3C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
3C Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
3C Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
[1]
SEQUENCE FROM N.A., AND SEQUENCE OF 208-247.
TISSUE=Lung;
MEDLINE=93170856; PubMed=8436402;
Lim B.L., Lu J., Reid K.B.M.;
"Structural similarity between bovine conglutinin and bovine lung
surfactant protein D and demonstration of liver as a site of
synthesis of conglutinin.";
Immunology 78:159-165(1993).
CC -!- FUNCTION: Contributes to the lung's defense against inhaled
microorganisms. Binds strongly maltose residues and to a lesser
extent other alpha-glucosyl moieties. It could participate in the
extracellular reorganization or turnover of pulmonary surfactant.
CC -!- SUBUNIT: Oligomeric complex of 4 set of homotrimers.
CC -!- SUBCELLULAR LOCATION: Extracellular.
CC -!- MISCELLANEOUS: Pulmonary surfactant consists of 90% lipid and 10%
protein. There are 4 surfactant-associated protein: 2 collagenous,
carbohydrate-binding glycoproteins (SP-A and SP-D) and 2 small
hydrophobic proteins (SP-B and SP-C).
CC -!- SIMILARITY: Contains 1 collagenous domain.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
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EMBL; X75911; CAA53510.1; -.
HSSP; P35247; 1B08.
InterPro; IPR008160; Collagen.
InterPro; IPR001304; Lectin_C.
Pfam; PF01391; Collagen; 2.
Pfam; PF00059; lectin_c; 1.
SMART; SM00034; CLECT; 1.
PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
PROSITE; PS00041; C_TYPE_LECTIN_2; 1.
Glycoprotein; Calcium; Surface film; Gaseous exchange; Hydroxylation;
Signal; Lectin; Collagen; Repeat; Coiled coil.
SIGNAL 1 20 BY SIMILARITY.
CHAIN 21 369 PULMONARY SURFACTANT-ASSOCIATED PROTEIN
D.
DOMAIN 46 216 COLLAGEN-LIKE.
COILED COIL (POTENTIAL).
DOMAIN 217 248 C-TYPE LECTIN (SHORT FORM).
DOMAIN 273 369 BY SIMILARITY.
DISULFID 275 367 BY SIMILARITY.
DISULFID 345 359 BY SIMILARITY.
CARBOHYD 90 90 N-LINKED (GLCNAC...) (POTENTIAL).
MOD_RES 78 78 HYDROXYLATION (BY SIMILARITY).
MOD_RES 87 87 HYDROXYLATION (BY SIMILARITY).
MOD_RES 96 96 HYDROXYLATION (BY SIMILARITY).
MOD_RES 99 99 HYDROXYLATION (BY SIMILARITY).
MOD_RES 165 165 HYDROXYLATION (BY SIMILARITY).
MOD_RES 171 171 HYDROXYLATION (BY SIMILARITY).
SEQUENCE 369 AA; 37361 MW; 07D8B24E0AE2E3 CRC64;
Query Match 20.0%; Score 83.5; DB 1; Length 369;
Best Local Similarity 25.3%; Pred. No. 0.049;
Matches 19; Conservative 16; Mismatches 39; Indels 1; Gaps 1;
QY 6 RETEEKFYIVQEEKNYRESLTHCRIRGGLAMPKDEAAANTLIADYVAKSGFFRVFIGV 65
DB 252 RSVGEKIFKTVGSEKTFQDAQOICQTAGGQLPSPRSGAENALTO-LATAQNKAAFLSMS 310
QY 66 DLREGQYIMTDNTP 80
DB 311 DTRKEGTFIVPTGEP 325
RESULT 4
```



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FT TURN 125 125
FT TURN 127 128
FT STRAND 130 140
FT TURN 140 140
FT TURN 141 142
FT STRAND 143 146
FT TURN 147 148
FT STRAND 151 151
FT STRAND 157 157
FT TURN 160 162
FT HELIX 168 170
FT STRAND 173 177
FT TURN 178 182
FT STRAND 183 187
FT TURN 189 190
FT STRAND 193 200
FT SEQUENCE 202 AA; 22567 MW; 280DCB5DF22E1AB8 CRC64;

Query Match 19.7%; Score 82; DB 1; Length 202;
Best Local Similarity 25.8%; Pred. No. 0.036;
Matches 17; Conservative 18; Mismatches 29; Indels 2; Gaps 1;

QY 11 KFYIVQEKYRSLTHCRIRGNLAMPKDEAANTLIADYVKS--GFRFVFIGVNDLE 68
DB 80 KCFLAFTQTKTFHEASEDCISRGCTLTPTQTSNDALVEYLRSQVGNRAEIVLGLNDMA 139
QY 69 REGQYMF 74
DB 140 REGTAV 145

RESULT 5
CL43_BOVIN STANDARD; PRT; 321 AA.
AC P42916; OBMF4;
DT 01-NOV-1995 (Rel. 32, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE Collectin-43 precursor (CL-43) (43 kDa collectin).
GN CL43.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=22414671; PubMed=12527419;
RA Hansen S., Holm D., Moeller V., Vitved L., Bendixen C., Skjodt K.,
RA Holmskov U.;
RT "Genomic and molecular characterization of CL-43 and its proximal
RT promoter.";
RL Biochim. Biophys. Acta 1625:1-10(2003).
RN [2]
RP SEQUENCE OF 21-321 FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=94216283; PubMed=8163480;
RA Lim B.-L., Willis A.C., Reid K.B.M., Lu J., Laursen S.B.,
RA Jensenius J.C., Holmskov U.;
RT "Primary structure of bovine collectin-43 (CL-43). Comparison with
RT conglutinin and lung surfactant protein-D.";
RL J. Biol. Chem. 269:11820-11824(1994).
CC -!- FUNCTION: Lectin that binds to various sugars: mannose = manNAc >
CC fucose > galNAc > glucose = maltose > galactose > lactose >
CC galNAc. Could play a role in immune defense.
CC -!- SUBUNIT: Oligomeric complex of 4 set of homotrimers.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Liver specific.
CC -!- PTM: Hydroxylated (Potential).
CC -!- SIMILARITY: Contains 1 collagenous domain.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
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CC -----
DR EMBL; AY071821; AAL61855.1; -.
DR EMBL; AY071822; AAL61856.1; -.
DR EMBL; X75912; CAA53511.1; ALT_SEQ.
DR HSSP; P35247; IB08.
DR InterPro; IPR008160; Collagen.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF01391; Collagen; 2.
DR Pfam; PF00059; Lectin_C; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C-TYPE LECTIN 1; 1.
DR PROSITE; PS00041; C-TYPE LECTIN 2; 1.
KW Lectin; Hydroxylation; Glycoprotein; Mannose-binding; Collagen;
KW Repeat; Calcium; signal.
FT SIGNAL 1 20
FT CHAIN 21 321 COLLECTIN-43.
FT DOMAIN 49 162 COLLAGEN-LIKE.
FT DOMAIN 222 321 C-TYPE LECTIN (SHORT FORM).
FT DISULFID 224 319 BY SIMILARITY.
FT DISULFID 297 311 BY SIMILARITY.
FT CONFLICT 125 125 T -> A (IN REF. 2).
FT CONFLICT 286 286 N -> G (IN REF. 2).
SQ SEQUENCE 321 AA; 33615 MW; 12BF120BB4861A1 CRC64;

Query Match 19.5%; Score 81.5; DB 1; Length 321;
Best Local Similarity 28.4%; Pred. No. 0.069;
Matches 19; Conservative 15; Mismatches 30; Indels 3; Gaps 2;

QY 10 EKFYIVQEKYRSLTHCRIRGNLAMPKDEAANTLIADYV-AKSGFRFVFIGVNDLE 68
DB 205 EKIFTAGVKSYSDAEQLCRAKQGLASPRSSAENAVTQLVRAKNK--HAYLSMNDIS 262
QY 69 REGQYMF 75
DB 263 KEGKFTY 269

RESULT 6
CL46_BOVIN STANDARD; PRT; 371 AA.
AC Q8NHZ9;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Collectin-46 precursor (CL-46) (46 kDa collectin).
GN CL46.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Hansen S., Holm D., Moeller V., Vitved L., Bendixen C., Reid K.B.M.,
RA Skjodt K., Holmskov U.;
RT "CL-46, a novel collectin highly expressed in the bovine thymus and
RT liver.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SUBUNIT: Oligomeric complex of 4 set of homotrimers (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Highly expressed in thymus and liver.
CC -!- PTM: Hydroxylated (Potential).
CC -!- SIMILARITY: Contains 1 collagenous domain.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
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CC -----  
CC DR EMBL; AF509589; AAM34742.1; --  
CC DR EMBL; AF509590; AAM34743.1; --  
CC DR InterPro; IPR008160; Collagen.  
CC DR InterPro; IPR001304; Lactin C.  
CC DR Pfam; PF01391; Collagen; 2.  
CC DR Pfam; PF00059; lectin c; 1.  
CC DR SMART; SM00034; CLECT; 1.  
CC DR PROSITE; PS00615; C-TYPE LECTIN 1; 1.  
CC DR PROSITE; PS00841; C-TYPE LECTIN 2; 1.  
CC KW Lactin; Hydroxylation; Glycoprotein; Mannose-binding; Membrane;  
CC KW Collagen; Repeat; Calcium; Signal.  
CC FT SIGNAL 1 20  
CC FT CHAIN 21 371  
CC FT DOMAIN 46 216  
CC FT DOMAIN 273 371  
CC FT SITE 201 303  
CC FT SITE 275 369  
CC FT DISULFID 347 361  
CC FT DISULFID 347 90  
CC FT CARBOHYD 90 90  
CC SQ SEQUENCE 371 AA; 37445 MW; 108AC45A91420E83 CRC64;

Query Match 19.5%; Score 81.5; DB 1; Length 371;  
Best Local Similarity 29.9%; Pred. No. 0.081;  
Matches 20; Conservative 14; Mismatches 30; Indels 3; Gaps 2;

QY 10 EKPYIVIOEKNYRESLTHCRIGRMGLAMPDEAAANTLIADYV-AKSGFFRVFVGVNDLE 68

Db 256 KXIFTAGVKSYSDAQQLCREAKGQASPSAAENEAVALVRKXN--DAFLSNMDS 313

QY 69 REGQYWF 75

Db 314 TEKGFTY 320

## RESULT 7

ID MANR HUMAN STANDARD; PRT; 1456 AA.  
AC P22897;  
DT 01-AUG-1991 (Rel. 19, Created)  
DT 01-AUG-1991 (Rel. 19, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Macrophage mannose receptor precursor (MWR) (CD206 antigen).  
GN MRC1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
RC TISSUE=Placenta;  
RX MEDLINE=90324192; PubMed=2373685;  
RA Taylor M.E., Conary J.T., Lennartz M.R., Stahl P.D., Drickamer K.;  
RT "Primary structure of the mannose receptor contains multiple motifs  
RT resembling carbohydrate-recognition domains.";  
RL J. Biol. Chem. 265:12156-12162 (1990).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=93052405; PubMed=1294118;  
RA Kim S.J., Ruiz N., Bezouska K., Drickamer K.;  
RT "Organization of the gene encoding the human macrophage mannose  
RT receptor (MRC1).";  
RL Genomics 14:721-727 (1992).  
RN [3]  
RP STUDIES ON THE BINDING OF INDIVIDUAL LECTIN DOMAINS.  
RX MEDLINE=92112893; PubMed=1730714;  
RA Taylor M.E., Bezouska K., Drickamer K.;

"Contribution to ligand binding by multiple carbohydrate-recognition  
domains in the macrophage mannose receptor.";  
J. Biol. Chem. 267:1719-1726 (1992).  
RN [4]  
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 642-788.  
RX MEDLINE=20347275; PubMed=10779515;  
RA Feinberg H., Park-Snyder S., Kolatkar A.R., Heise C.T., Taylor M.E.,  
RA Weiss W.I.;  
RT "Structure of a C-type carbohydrate recognition domain from the  
RT macrophage mannose receptor.";  
RL J. Biol. Chem. 275:21539-21548 (2000).  
CC -!- FUNCTION: Mediates the endocytosis of glycoproteins by  
CC macrophages, in several recognition and uptake processes.  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -!- MISCELLANEOUS: CRDs 1-3 have at most very weak affinity for  
CC carbohydrate. CRD 4 shows the highest affinity binding and has  
CC multispecificity for a variety of monosaccharides. At least 3 CRDs  
CC (4, 5, and 7) are required for high affinity binding and  
CC endocytosis of multivalent glycoconjugates.  
CC -!- SIMILARITY: Contains 8 C-type lectin family domains.  
CC -!- SIMILARITY: Contains 1 ricin B-type lectin domain.  
CC -!- DATABASE: NAME=PROW; NOTE=PROW 2:85-89 (2001);  
CC WWW="http://www.ncbi.nlm.nih.gov/prow/guide/1644341535\_g.htm".  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC -----  
CC EMBL; J05550; AAA59868.1; --  
CC EMBL; M93221; AAA60389.1; --  
CC EMBL; M93192; AAA60389.1; JOINED.  
CC EMBL; M93193; AAA60389.1; JOINED.  
CC EMBL; M93194; AAA60389.1; JOINED.  
CC EMBL; M93195; AAA60389.1; JOINED.  
CC EMBL; M93196; AAA60389.1; JOINED.  
CC EMBL; M93197; AAA60389.1; JOINED.  
CC EMBL; M93198; AAA60389.1; JOINED.  
CC EMBL; M93199; AAA60389.1; JOINED.  
CC EMBL; M93200; AAA60389.1; JOINED.  
CC EMBL; M93201; AAA60389.1; JOINED.  
CC EMBL; M93202; AAA60389.1; JOINED.  
CC EMBL; M93203; AAA60389.1; JOINED.  
CC EMBL; M93204; AAA60389.1; JOINED.  
CC EMBL; M93205; AAA60389.1; JOINED.  
CC EMBL; M93206; AAA60389.1; JOINED.  
CC EMBL; M93207; AAA60389.1; JOINED.  
CC EMBL; M93208; AAA60389.1; JOINED.  
CC EMBL; M93209; AAA60389.1; JOINED.  
CC EMBL; M93210; AAA60389.1; JOINED.  
CC EMBL; M93211; AAA60389.1; JOINED.  
CC EMBL; M93212; AAA60389.1; JOINED.  
CC EMBL; M93213; AAA60389.1; JOINED.  
CC EMBL; M93214; AAA60389.1; JOINED.  
CC EMBL; M93215; AAA60389.1; JOINED.  
CC EMBL; M93216; AAA60389.1; JOINED.  
CC EMBL; M93217; AAA60389.1; JOINED.  
CC EMBL; M93218; AAA60389.1; JOINED.  
CC EMBL; M93219; AAA60389.1; JOINED.  
CC EMBL; M93220; AAA60389.1; JOINED.  
CC PIR; A36563; A36563.  
CC PDB; 1EGG; 30-AUG-00.  
CC PDB; 1EG1; 30-AUG-00.  
CC Genew; HGNC:7229; MRC1.  
CC MIM; 153618; --  
CC GO; GO:0005887; C:integral to plasma membrane; TAS.  
CC GO; GO:0005537; F:mannose binding; TAS.  
CC GO; GO:0004872; F:receptor activity; TAS.  
CC GO; GO:0006898; P:receptor mediated endocytosis; TAS.  
CC InterPro; IPR002353; Antifreeze1.

DR InterPro; IPR000562; FN Type II.  
DR InterPro; IPR001304; LECTIN C.  
DR InterPro; IPR000772; Ricin\_B\_lectin.  
DR InterPro; IPR008997; RicinB\_like.  
DR Pfam; PF00040; fn2; 1.  
DR Pfam; PF00059; lectin\_C; 8.  
DR Pfam; PF00652; Ricin\_B\_lectin; 2.  
DR PRINTS; PR00356; ANTIFFREEZEII.  
DR PRINTS; PR00013; FNTYPEII.  
DR ProDom; PD000995; FN Type\_II; 1.  
DR SMART; SM00034; CLECT; 8.  
DR SMART; SM00059; FN2; 1.  
DR SMART; SM00458; RICIN; 1.  
DR PROSITE; PS00615; C-TYPE\_LECTIN\_1; 6.  
DR PROSITE; PS00041; C-TYPE\_LECTIN\_2; 8.  
DR PROSITE; PS00023; FIBRONECTIN\_2; 1.  
DR PROSITE; PS00231; RICIN\_B\_LECTIN; 1.  
KW Receptor; Signal; Calcium-binding; Transmembrane; Repeat;  
KW Glycoprotein; Endocytosis; Macrophage; Lectin; Antigen; 3D-structure.  
FT SIGNAL 1 18  
FT CHAIN 19 1456  
FT DOMAIN 19 1383  
FT TRANSMEM 1384 1411  
FT DOMAIN 1412 1456  
FT DOMAIN 22 142  
FT DOMAIN 157 212  
FT DOMAIN 216 344  
FT DOMAIN 360 629  
FT DOMAIN 644 781  
FT DOMAIN 805 926  
FT DOMAIN 943 1083  
FT DOMAIN 1100 1216  
FT DOMAIN 1228 1359  
FT DISULFID 646 659  
FT DISULFID 680 777  
FT DISULFID 753 769  
FT CARBOHYD 104 344  
FT CARBOHYD 344 344  
FT CARBOHYD 529 529  
FT CARBOHYD 926 926  
FT CARBOHYD 930 930  
FT CARBOHYD 1160 1160  
FT CARBOHYD 1205 1205  
FT CARBOHYD 1311 1311  
FT TURN 648 649  
FT STRAND 651 652  
FT TURN 654 655  
FT STRAND 658 663  
FT STRAND 667 669  
FT STRAND 671 671  
FT HELIX 673 683  
FT TURN 684 684  
FT STRAND 686 687  
FT HELIX 693 705  
FT TURN 706 707  
FT TURN 709 710  
FT STRAND 712 718  
FT TURN 723 724  
FT STRAND 727 727  
FT TURN 729 730  
FT STRAND 733 733  
FT TURN 741 742  
FT HELIX 746 748  
FT STRAND 752 757  
FT TURN 758 761  
FT STRAND 764 768  
FT TURN 769 770  
FT STRAND 773 780  
FT TURN 781 782  
SQ SEQUENCE 1456 AA; 165011 MW; 264E5AF3C576A5E3 CRC64;  
19.5%; Score 81.5; DB 1; Length 1456;

Query Match

Best Local Similarity 28.8%; Pred. No. 0.39;  
Matches 19; Conservative 15; Mismatches 31; Indels 1; Gaps 1;  
QY 12 FYIVQEKXNYRESLTHCRIRGMLAMPKDEANTLIADYAKSGFFRVFVIGVNDLREG 71  
Db 960 FGWEERKNQKQKACIGFQGNLVISIQNEQAFILT-YHMKDSTFFSAWTGLNDVNSEH 1018  
QY 72 QYMFTD 77  
Db 1019 TFLWTD 1024  
RESULT 8  
PSPD\_MOUSE  
ID PSPD\_MOUSE STANDARD; PRT; 374 AA.  
AC PS0404;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DT Pulmonary surfactant-associated protein D precursor (SP-D) (PSP-D).  
GN SFTPD OR SFTPD4.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6 X CBA; TISSUE=Lung;  
RA MEDLINE=96094460; PubMed=7499882;  
RA Motwani M., White R.A., Guo N., Dowler L.L., Tauber A.I., Sastry K.N.;  
RT "Mouse surfactant protein-D. cDNA cloning, characterization, and gene  
localization to chromosome 14.";  
RL J. Immunol. 155:5671-5677(1995).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=129/SV;  
RX MEDLINE=99244602; PubMed=10226065;  
RA Lawson P.R., Perkins V.C., Holmskov U., Reid K.B.;  
RT "Genomic organization of the mouse gene for lung surfactant protein  
D.";  
RL Am. J. Respir. Cell Mol. Biol. 20:953-963(1999).  
RN [3]  
RP SEQUENCE FROM N.A.  
RA Fisher J.H., Sheftelyevich V.V.;  
RT "Surfactant protein-D regulates surfactant phospholipid homeostasis in  
vivo.";  
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,  
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler N.K.,  
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
Stapleton M., Soares M.B., Bonaldo M.F., Carninci P., Scheetz T.E.,  
Brownstein W.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,  
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length  
human and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
CC -!- FUNCTION: Contributes to the lung's defense against inhaled  
microorganisms. Binds strongly maltose residues and to a lesser  
extent other alpha-glucosyl moieties. It could participate in the



CC extracellular reorganization or turnover of pulmonary surfactant.  
 CC -!- SUBUNIT: Oligomeric complex of 4 set of homotrimers.  
 CC -!- SUBCELLULAR LOCATION: Extracellular.  
 CC -!- MISCELLANEOUS: Pulmonary surfactant consists of 90% lipid and 10%  
 CC protein. There are 4 surfactant-associated protein: 2 collagenous,  
 CC carbohydrate-binding glycoproteins (SP-A and SP-D) and 2 small  
 CC hydrophobic proteins (SP-B and SP-C).  
 CC -!- SIMILARITY: Contains 1 collagenous domain.  
 CC -!- SIMILARITY: Contains 1 C-type lectin family domain.  
 CC  
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 CC  
 CC EMBL; L40156; AAA92021.1; -.  
 CC EMBL; AF047742; AAD31380.1; -.  
 CC EMBL; AF047741; AAD31380.1; JOINED.  
 CC EMBL; AF192134; AAF15277.1; -.  
 CC EMBL; BC003705; AAH03705.1; -.  
 CC HSP; F35247; I808.  
 CC MGD; MG1:109515; Sftpd.  
 CC InterPro; IPR008160; Collagen.  
 CC InterPro; IPR001304; Lectin C.  
 CC Pfam; PF01391; Collagen; 3.  
 CC Pfam; PF00059; lectin c; 1.  
 CC Pfam; PF00034; CLECT; 1.  
 CC SMART; SM00034; CLECT; 1.  
 CC PROSITE; PS00615; C-TYPE LECTIN 1; 1.  
 CC PROSITE; PS50041; C-TYPE LECTIN 2; 1.  
 CC Glycoprotein; Calcium; Surface film; Gaseous exchange; Hydroxylation;  
 CC Signal; Lectin; Collagen; Repeat; Coiled coil.  
 CC SIGNAL 1  
 CC BY SIMILARITY.  
 CC CHAIN 19  
 CC PULMONARY SURFACTANT-ASSOCIATED PROTEIN  
 CC D.  
 CC DOMAIN 45 221  
 CC COLLAGEN-LIKE.  
 CC COILED COIL (POTENTIAL).  
 CC DOMAIN 222 253  
 CC C-TYPE LECTIN (SHORT FORM).  
 CC DOMAIN 278 374  
 CC BY SIMILARITY.  
 CC DISULFID 280 372  
 CC BY SIMILARITY.  
 CC DISULFID 350 364  
 CC BY SIMILARITY.  
 CC CARBOHYD 89  
 CC N-LINKED (GLCNAC... ) (POTENTIAL).  
 CC SEQUENCE 374 AA; 37688 MW; FE034261263F43E4 CRC64;  
 CC  
 CC Query Match 19.1%; Score 79.5; DB 1; Length 374;  
 CC Best Local Similarity 22.7%; Pred. No. 0.14;  
 CC Matches 17; Conservative 14; Mismatches 43; Indels 1; Gaps 1;  
 CC  
 CC 6 RETEEKYVYQEEKKYRESLTHCRINGGMLMPKDEAANTLIADYVAKSGFRVFIGVN 65  
 CC 257 RSVGDKIFRTADSEKPEDAQEMCKQAGQLASPRGATENAIIQLITAHN-KAAPLSMT 315  
 CC  
 CC 66 DLREGQYMTDNTF 80  
 CC 316 DVGTGKFTYPTGEP 330  
 CC  
 CC RESULT 9  
 CC PSPA\_HUMAN  
 CC STANDARD; PRT; 248 AA.  
 CC P07714;  
 CC 01-APR-1988 (Rel. 07, Created)  
 CC 01-APR-1990 (Rel. 14, Last sequence update)  
 CC 28-FEB-2003 (Rel. 41, Last annotation update)  
 CC Pulmonary surfactant-associated protein A precursor (SP-A) (PSP-A)  
 CC (PSPAP) (Alveolar proteinosis protein) (35 kDa pulmonary surfactant-  
 CC associated protein).  
 CC (SFTPA1 OR SFTPA OR SFTP1 OR PSPAP) AND (SFTPA2 OR SFTPA).  
 CC Homo sapiens (Human).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 CC NCBI\_taxid=9606;  
 CC

RP SEQUENCE FROM N.A.  
 RX MEDLINE=86250832; PubMed=3755136;  
 RA Floros J., Steinbrink R., Jacobs K., Phelps D., Kriz R., Recny M.,  
 RA Sultzman L., Jones S., Tausch H.W., Frank H.A., Fritsch E.F.,  
 "Isolation and characterization of cDNA clones for the 35-kDa  
 FT pulmonary surfactant-associated protein.",  
 RL J. Biol. Chem. 261:9029-9033 (1986).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=86014366; PubMed=299582;  
 RA White R.T., Damm D., Miller J., Spratt K., Schilling J., Hawgood S.,  
 RA Benson B., Cordell B.;  
 FT "Isolation and characterization of the human pulmonary surfactant  
 RT apoprotein gene.",  
 RL Nature 317:361-363 (1985).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92198680; PubMed=1372511;  
 RA Katyal S.L., Singh G., Locker J.L.;  
 FT "Characterization of a second human pulmonary surfactant-associated  
 RT protein SP-A gene.",  
 RL Am. J. Respir. Cell Mol. Biol. 6:446-452 (1992).  
 CC -!- FUNCTION: In presence of calcium ions, PSAP binds to surfactant  
 CC phospholipids and contributes to lower the surface tension at the  
 CC air-liquid interface in the alveoli of the mammalian lung and is  
 CC essential for normal respiration.  
 CC -!- SUBUNIT: Oligomeric complex of 6 set of homotrimers.  
 CC -!- SUBCELLULAR LOCATION: Extracellular.  
 CC -!- MISCELLANEOUS: Pulmonary surfactant consists of 90% lipid and 10%  
 CC protein. There are 4 surfactant-associated protein: 2 collagenous,  
 CC carbohydrate-binding glycoproteins (SP-A and SP-D) and 2 small  
 CC hydrophobic proteins (SP-B and SP-C).  
 CC -!- SIMILARITY: Contains 1 collagenous domain.  
 CC -!- SIMILARITY: Contains 1 C-type lectin family domain.  
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 CC  
 CC EMBL; M13686; AAA60211.1; -.  
 CC EMBL; K03475; AAA36520.1; -.  
 CC EMBL; M30838; AAA36510.1; -.  
 CC EMBL; M68519; AAA60319.1; -.  
 CC PIR; A25720; LNHUP6.  
 CC HSP; P22897; LEGG.  
 CC Genew; HGNC:10798; SFTPA1.  
 CC Genew; HGNC:10799; SFTPA2.  
 CC MIN; 178630; -.  
 CC MIN; 178642; -.  
 CC GO; GO:0005319; Filopid transporter activity; TAS.  
 CC InterPro; IPR008160; Collagen.  
 CC InterPro; IPR001304; Lectin C.  
 CC Pfam; PF01391; Collagen; 2.  
 CC Pfam; PF00059; lectin c; 1.  
 CC SMART; SM00034; CLECT; 1.  
 CC PROSITE; PS00615; C-TYPE LECTIN 1; 1.  
 CC PROSITE; PS50041; C-TYPE LECTIN 2; 1.  
 CC Glycoprotein; Calcium; Surface film; Gaseous exchange; Hydroxylation;  
 CC Signal; Lectin; Collagen; Repeat; Polymorphism.  
 CC SIGNAL 1  
 CC CHAIN 21 248  
 CC PULMONARY SURFACTANT-ASSOCIATED PROTEIN  
 CC A.  
 CC DOMAIN 28 100  
 CC COLLAGEN-LIKE.  
 CC C-TYPE LECTIN (SHORT FORM).  
 CC DOMAIN 153 248  
 CC BY SIMILARITY.  
 CC DISULFID 155 246  
 CC DISULFID 224 238  
 CC BY SIMILARITY.  
 CC CARBOHYD 207 207  
 CC N-LINKED (GLCNAC... ) (PROBABLE).  
 CC VARIANT 9  
 CC N -> T.





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CC -----

DR EMBL; AB009246; BAA32406.1; -;  
DR HSP; P05452; 1HTN.  
DR GO; GO:0005576; C:extracellular; IDA.  
DR GO; GO:0008083; F:growth factor activity; IDA.  
DR GO; GO:0005529; F:sugar binding; NAS.  
DR GO; GO:0008284; F:positive regulation of cell proliferation; IDA.  
DR InterPro; IPR001304; Lectin\_C.  
DR Pfam; PF00059; lectin\_c; 1.  
DR SMART; SM00034; CLECT; 1.  
DR PROSITE; PS00615; C-TYPE LECTIN 1; 1.  
DR PROSITE; PS00411; C-TYPE LECTIN 2; 1.  
DR Growth factor; Glycoprotein; Lectin; Signal.  
KW SIGNAL  
FT CHAIN 1 21  
FT DOMAIN 22 328 STEM CELL GROWTH FACTOR.  
FT DOMAIN 188 325 C-TYPE LECTIN.  
SQ SEQUENCE 328 AA; 36387 MW; C115188AC23D6257 CRC64;

Query Match 18.7%; Score 78; DB 1; Length 328;  
Best Local Similarity 27.3%; Pred. No. 0.18; Indels 4; Gaps 3;  
Matches 21; Conservative 19; Mismatches 33; Indels 4; Gaps 3;

QY 2 IAGIRETEKFFYIVQEKYKRESLTHCRINGGMLAMPKDAANTLIADYV--AKSGP-F 58  
DB 183 LKGLR-LGHKCFLLSRDPTQAAQAKRGGLGSLAQPADRQMDALSRYLAALAPYNN 241

QY 59 RVFIGVNDLEREGQMP 75  
DB 242 PVLGVHRRSEGLYLF 258

RESULT 13  
ID KUOR RAT STANDARD; PRT; 550 AA.  
AC P10716;  
DT 01-APR-1990 (Rel. 14, Created)  
DT 01-APR-1990 (Rel. 14, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE C-type lectin 13 (Kupffer cell receptor).  
GN CLESP13 OR KCLR.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
SQ SEQUENCE FROM N.A., AND SEQUENCE OF 83-104.  
RA MEDLINE=88227939; PubMed=2836387;  
RA Hoyle G.W., Hill R.L.;  
RA "Molecular cloning and sequencing of a cDNA for a carbohydrate  
RT binding receptor unique to rat Kupffer cells.";  
RL J. Biol. Chem. 263:7487-7492(1988).  
RN [2]

RP SEQUENCE FROM N.A.  
RX MEDLINE=91107689; PubMed=1846367;  
RA Hoyle G.W., Hill R.L.;  
RA "Structure of the gene for a carbohydrate-binding receptor unique to  
RT rat Kupffer cells.";  
RL J. Biol. Chem. 266:1850-1857(1991).  
CC -!- FUNCTION: Receptor with an affinity for galactose and fucose.  
CC Could be involved in endocytosis.  
CC -!- SUBCELLULAR LOCATION: Type II membrane protein.  
CC -!- TISSUE SPECIFICITY: Kupffer cells.  
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.  
CC -----

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DR EMBL; J03734; AAA41472.1; -;  
DR EMBL; M5532; AAA40892.1; -;  
DR PIR; A38674; A28166.  
DR HSP; P20693; IHLJ.  
DR InterPro; IPR002353; AntifreezeII.  
DR InterPro; IPR001304; Lectin\_C.  
DR Pfam; PF00059; lectin\_c; 1.  
DR PRINTS; PR00356; ANTIFREEZEII.  
DR SMART; SM00034; CLECT; 1.  
DR PROSITE; PS00615; C-TYPE LECTIN 1; 1.  
DR PROSITE; PS00411; C-TYPE LECTIN 2; 1.  
KW Receptor; Transmembrane; Glycoprotein; Lectin; Signal-anchor;  
KW Endocytosis.  
FT DOMAIN 1 42 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 43 69 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)  
(POTENTIAL).  
FT DOMAIN 70 550 EXTRACELLULAR (POTENTIAL).  
FT DOMAIN 438 538 C-TYPE LECTIN (SHORT FORM).  
FT DISULFID 440 536 BY SIMILARITY.  
FT DISULFID 516 528 BY SIMILARITY.  
FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 93 93 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 115 115 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 132 132 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 209 209 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 255 255 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 550 AA; 61104 MW; 9358A6CF4C306270 CRC64;

Query Match 18.8%; Score 77.5; DB 1; Length 550;  
Best Local Similarity 27.1%; Pred. No. 0.36;  
Matches 19; Conservative 14; Mismatches 34; Indels 3; Gaps 1;  
QY 11 KFYIVQEEKYKRESLTHCRINGGMLAMPKDAANTLIADYVAKSGFPRFVIGVNDLERE 70  
DB 422 KFYFSDKSWHEAENFCVSGAHLASVTSQEQAFL--VQITNAVDFHIGLTDQGT 478  
QY 71 QGYMFTDTP 80  
DB 479 GNRWVDGTP 488

RESULT 14  
ID CONG\_BOVIN STANDARD; PRT; 371 AA.  
AC P23805; O97748;  
DT 01-NOV-1991 (Rel. 20, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 01-OCT-1996 (Rel. 34, Last annotation update)  
DE Conglutinin precursor.  
GN CGN1.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=93213261; PubMed=8460993;  
RA Suzuki Y., Yin J., Makino M., Kurimura T., Wakamiya N.;  
RT "Cloning and sequencing of a cDNA coding for bovine conglutinin.";  
RL Biochem. Biophys. Res. Commun. 191:335-342(1993).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=93277452; PubMed=7684896;  
RA Lu J., Laursen S.B., Thiel S., Jensenius J.C., Reid B.M.;  
RT "The cDNA cloning of conglutinin and identification of liver as a  
RT primary site of synthesis of conglutinin in members of the Bovidae.";

Biochem. J. 292:157-162(1993).  
[3]  
SEQUENCE FROM N.A.  
TISSUE=Liver;  
MEDLINE=94215917; PubMed=8163202;  
RA Liou L.S., Sastry R., Hartshorn K.L., Lee Y.M., Okarma T.B.,  
Tauber A.I., Sastry K.N.;  
RT "Bovine conglutinin (BC) mRNA expressed in liver: cloning and  
RT characterization of the BC cDNA reveals strong homology to surfactant  
RT protein-D";  
RL Gene 141:277-281(1994).  
[4]  
SEQUENCE FROM N.A.  
TISSUE=Semen;  
MEDLINE=94267222; PubMed=8207234;  
RA Liou L.S., Sastry R., Hartshorn K.L., Lee Y.M., Okarma T.B.,  
Tauber A.I., Sastry K.N.;  
RT "Bovine conglutinin gene exon structure reveals its evolutionary  
RT relationship to surfactant protein-D";  
RL J. Immunol. 153:173-180(1994).  
[5]  
SEQUENCE FROM N.A.  
TISSUE=Liver;  
MEDLINE=94128104; PubMed=8297370;  
RA Kawasaki N., Itoh N., Kawasaki T.;  
RT "Gene organization and 5'-flanking region sequence of conglutinin: a  
RT C-type mammalian lectin containing a collagen-like domain";  
RL Biochem. Biophys. Res. Commun. 198:597-604(1994).  
[6]  
SEQUENCE OF 21-371.  
MEDLINE=91131556; PubMed=1993651;  
RA Lee Y.-W., Leiby K.R., Allar J., Paris K., Lerch B., Okarma T.B.;  
RT "Primary structure of bovine conglutinin, a member of the C-type  
RT animal lectin family";  
RL J. Biol. Chem. 266:2715-2723(1991).  
[7]  
PRELIMINARY SEQUENCE OF 21-52.  
MEDLINE=87184551; PubMed=3566740;  
RA Young N.M., Jeon M.A.;  
RT "The carbohydrate specificity of conglutinin and its homology to  
RT proteins in the hepatic lectin family";  
RL Biochem. Biophys. Res. Commun. 143:645-651(1987).  
CC -!- FUNCTION: Calcium-dependent lectin-like protein which binds to a  
CC yeast cell wall extract and immune complexes through the  
CC complement component (C3bi). It is capable of binding nonreducing  
CC terminal N-acetylglucosamine, mannose, and fucose residues.  
CC -!- SUBUNIT: Oligomeric complex of 4 set of homotrimers.  
CC -!- SIMILARITY: Contains 1 collagenous domain.  
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
XR EMBL; D14085; BAA03170.1; -  
XR EMBL; X71774; CAA50665.1; -  
XR EMBL; L18871; AAA20126.1; -  
XR EMBL; U06860; AAB60624.1; -  
XR EMBL; U06854; AAB60624.1; JOINED.  
XR EMBL; U06855; AAB60624.1; JOINED.  
XR EMBL; U06856; AAB60624.1; JOINED.  
XR EMBL; U06857; AAB60624.1; JOINED.  
XR EMBL; U06858; AAB60624.1; JOINED.  
XR EMBL; U06859; AAB60624.1; JOINED.  
XR EMBL; D25302; BAA04983.2; -  
XR EMBL; D25296; BAA04983.2; JOINED.  
XR EMBL; D25297; BAA04983.2; JOINED.  
XR EMBL; D25298; BAA04983.2; JOINED.  
XR EMBL; D25299; BAA04983.2; JOINED.

DR EMBL; D25300; BAA04983.2; JOINED.  
DR EMBL; D25301; BAA04983.2; JOINED.  
DR PIR; I45878; I45878.  
DR PIR; JN0450; JN0450.  
DR HSSP; P35247; 1808.  
DR InterPro; IPR008161; Clg\_helix.  
DR InterPro; IPR008160; Collagen.  
DR InterPro; IPR001304; Lectin\_C.  
DR Pfam; PF01391; Collagen; 3.  
DR Pfam; PF00059; Lectin\_C; 1.  
DR ProDom; PD000007; Clg\_helix; 1.  
DR SMART; SM00034; CLEC; 1.  
DR PROSITE; PS00615; C-TYPE LECTIN 1; 1.  
DR PROSITE; PS50041; C-TYPE LECTIN 2; 1.  
KW Lectin; Hydroxylation; Glycoprotein; Mannose-binding; Membrane;  
KW Collagen; Repeat; Calcium; Signal.  
FT SIGNAL 1 20 CONGLUTININ.  
FT CHAIN 21 371 COLLAGEN-LIKE.  
FT DOMAIN 46 216 C-TYPE LECTIN (SHORT FORM).  
FT DOMAIN 273 371 HYDROXYLATION.  
FT MOD\_RES 63 63 HYDROXYLATION.  
FT MOD\_RES 87 87 HYDROXYLATION.  
FT MOD\_RES 99 99 HYDROXYLATION.  
FT MOD\_RES 135 135 HYDROXYLATION.  
FT MOD\_RES 141 141 HYDROXYLATION.  
FT MOD\_RES 159 159 HYDROXYLATION.  
FT MOD\_RES 162 162 HYDROXYLATION.  
FT MOD\_RES 198 198 HYDROXYLATION.  
FT SITE 201 203 CELL ATTACHMENT SITE (POTENTIAL).  
FT DISULFID 275 369 BY SIMILARITY.  
FT CARBOHYD 337 337 N-LINKED (GLCNAC... ) (POTENTIAL).  
FT CONFLICT 173 173 R -> H (IN REF. 2 AND 3).  
FT CONFLICT 210 210 K -> S (IN REF. 6).  
FT CONFLICT 218 218 V -> A (IN REF. 2).  
FT CONFLICT 272 272 E -> V (IN REF. 2).  
SQ SEQUENCE 371 AA; 37594 MW; 867EB41992544B1F CRC64;  
Query Match 18.3%; Score 76.5; DB 1; Length 371;  
Best Local Similarity 25.8%; Pred. No. 0.3;  
Matches 17; Conservative 15; Mismatches 33; Indels 1; Gaps 1;  
Qy 10 EKQYVIOEKYRESLTHCRTRGGGLAMPKDEANTLIADYVAKSGFRVFIGVNDLER 69  
Db 256 EKIFTAGAVKSYSDAEQLCREAKGOLASPRSSAENEAVTQMV-PAQKNAYLSMNDIST 314  
Qy 70 EGQYMF 75  
Db 315 EGRFTY 320  
RESULT 15  
KUCR MOUSE  
ID KUCR MOUSE STANDARD; PRT; 548 AA.  
AC P70194;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE C-type lectin 13 (Kupffer cell receptor).  
GN CLECSF13 OR KCLR.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BALB/c; TISSUE=Liver;  
RA Takezawa R., Wagatsuma H., Nomoto C., Watanabe Y., Akaike T.;  
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=FVB/N; TISSUE=Liver;  
RL MEDLINE=22388257; PubMed=12477932;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
Klausner R.D., Collins F.S., Wagner L., Schenken C.F., Schuler G.D.,  
Altshuler S.D., Zeeberg E., Buetow K.H., Schafer C.M., Bhat N.K.,  
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
Stapleton M.J., Soares M.B., Bonaldo M.F., Casavant P., Scheetz T.E.,  
Brownstein M.J., Usdin T.B., Tohiyuki S., Carninci P., Prange C.,  
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
Fahey J., Helton E., Ketteman M., Madan A.C., Rodrigues S., Sanchez A.,  
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
"Generation and initial analysis of more than 15,000 full-length  
human and mouse cDNA sequences.";  
*Proc. Natl. Acad. Sci. U.S.A.* 99:16899-16903(2002).  
-!- FUNCTION: Receptor with an affinity for galactose and fucose.  
Could be involved in endocytosis.  
-!- SUBCELLULAR LOCATION: Type II membrane protein.  
-!- TISSUE SPECIFICITY: Kupffer cells.  
-!- SIMILARITY: Contains 1 C-type lectin family domain.  
-----  
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or send an email to [license@isb-eib.ch](mailto:license@isb-eib.ch)).  
-----  
EMBL; D88577; BAAL3647.1; --  
EMBL; BC013647; AAH3647.1; --  
DR HSSP; P20693; IHLJ.  
DR MGD; MG1:1859834; Clecslf13.  
DR InterPro; IPR002353; AntifreezeZell.  
DR InterPro; IPR001304; Lectin C.  
DR Pfam; PF00059; lectin\_c\_1.  
DR PRINTS; PR00356; ANTIFREEZEII.  
DR SMART; SM00034; CLECT\_1.  
DR PROSITE; PS00615; C\_TYPE\_LECTIN\_1; 1.  
DR PROSITE; PS00041; C\_TYPE\_LECTIN\_2; 1.  
KW Receptor; Transmembrane; Glycoprotein; Lectin; Signal-anchor;  
Endocytosis.  
FT DOMAIN 1 42 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 43 69 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)  
FT FT (POTENTIAL).  
FT DOMAIN 70 548 EXTRACELLULAR (POTENTIAL).  
FT DOMAIN 438 538 C-TYPE LECTIN (SHORT FORM).  
FT DISULFID 440 536 BY SIMILARITY.  
FT DISULFID 516 528 BY SIMILARITY.  
FT CARBOHYD 86 86 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 92 92 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 115 115 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 132 132 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 209 209 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 255 255 N-LINKED (GLCNAC. .) (POTENTIAL).  
SQ SEQUENCE 548 AA; 61268 MW; 6F6495B820E73BD9 CRC64;

Query Match 18.3%; Score 76.5; DB 1; Length 548;  
Best Local Similarity 26.1%; Pred. No. 0.47;  
Matches 18; Conservative 13; Mismatches 35; Indels 3; Gaps 1;

QY 12 FYIIVQEKNKYRESITLCRIIRGGMPLMKPEAAANTIADYVAKSQFFRVFIQGNLBREG 71  
Db 423 FYIFERDKXFWREAKFKFTCSGAHLASVTQSEQAFLVQTTSQGH---WIGLTDOGTGG 479

QY 72 QYNFDINTP 80  
Db 480 IWRMVDGTP 488

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 8, 2004, 12:03:01 ; Search time 21.1454 Seconds  
(without alignments)  
363.925 Million cell updates/sec

Title: US-09-600-932-2\_COPY\_148\_227

Perfect score: 417

Sequence: 1 VIAGIRETEKFFYIVQEEK.....FIGVNDLEREGQYMTDNT 80

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: PIR 78:\*

1: Pir1:\*

2: Pir2:\*

3: Pir3:\*

4: Pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	405	97.1	277	2 JC7903	collectin liver 1
2	91	21.8	166	1 A37289	tetranectin homolo
3	89.5	21.2	404	2 A45274	HIV gp120-binding
4	83.5	20.0	369	2 S3803	surfactant protein
5	82.5	19.8	1326	2 B56395	secretory phosphol
6	82.5	19.8	1465	2 A56395	secretory phosphol
7	82	19.7	202	1 TTHUN	tetranectin precur
8	82	19.7	321	2 T19259	hypothetical prote
9	81.5	19.5	301	2 A53570	collectin-43 - bov
10	81.5	19.5	1456	1 A36563	mannose receptor p
11	78.5	18.8	248	1 LNHUPS	pulmonary surfacta
12	78.5	18.8	248	1 LNHUP6	pulmonary surfacta
13	78.5	18.8	248	1 LNHUP1	pulmonary surfacta
14	78.5	18.8	248	2 I51921	pulmonary surfacta
15	78	18.7	202	2 JC4031	tetranectin precur
16	78	18.7	321	2 T36152	hypothetical prote
17	77.5	18.6	550	2 A28166	Kupffer cell recep
18	76.5	18.3	371	1 JN0450	conglutinin precu
19	76.5	18.3	371	2 I45878	conglutinin - bovi
20	74.5	17.9	1479	2 T42710	mannose receptor,
21	74	17.7	238	1 LNR7MA	mannose-binding le
22	73.5	17.6	155	2 S78774	perlucin - Haloti
23	73	17.5	321	2 T36153	hypothetical prote
24	71.5	17.1	374	1 A42046	surfactant protein
25	71.5	17.1	1450	2 T30273	hypothetical prote
26	71.5	17.1	1487	2 S48719	phospholipase-A(2)
27	70.5	16.9	331	1 S34198	IgE Fc receptor II
28	70.5	16.9	309	1 LNM5ER	IgE Fc receptor, I
29	70.5	16.9	1458	1 A49707	phospholipase A2 r

30 69.5 16.7 162 1 LNRC1 lectin BRA3-1 prec  
31 69.5 16.7 162 1 LNRC3 lectin BRA3-2 prec  
32 69.5 16.7 188 2 I59421 mast cell function  
33 69.5 16.7 317 2 AB0281 probable exported  
34 69.5 16.7 1463 2 A53210 phospholipase A2 r  
35 69 16.5 107 2 F83522 hypothetical prote  
36 69 16.5 330 2 T46256 brevicin - human (  
37 69 16.5 828 1 D39142 outer membrane ush  
38 68.5 16.4 2890 2 F64669 DNA-directed RNA p  
39 68 16.3 705 2 T18547 flax rust resistan  
40 68 16.3 1294 2 T18546 flax rust resistan  
41 67.5 16.2 314 2 AC0683 probable exported  
42 67 16.1 237 2 JC7608 type II lectin-lik  
43 66.5 15.9 375 1 A45225 pulmonary surfacta  
44 66.5 15.9 872 2 S55940 telomerase compone  
45 66.5 15.9 1455 1 A48925 mannose receptor p

## ALIGNMENTS

### RESULT 1

JC7903  
collectin liver 1 - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 03-Feb-2003 #sequence\_revision 03-Feb-2003 #text\_change 31-Mar-2003  
C:Accession: JC7903  
R:Kawai, T.; Suzuki, Y.; Eda, S.; Kase, T.; Ohtani, K.; Sakai, Y.; Keshi, H.; Fukuh, A  
Biosci. Biotechnol. Biochem. 66, 2134-2145, 2002.  
A:Title: Molecular cloning of mouse collectin liver 1.  
A:Reference number: JC7903; MUID:22333927; PMID:12450124  
A:Accession: JC7903  
A:Molecule type: mRNA  
A:Residues: 1-277 <RAW>  
A:Cross-references: DDBJ:AB016429  
A:Experimental source: liver  
A:Comment: This protein is a highly conserved cytosolic protein and belongs to a verteb:  
c development.  
C:Genetics:  
A:Gene: C11  
A:Map position: 15

### Query Match

Best Local Similarity 97.1%; Score 405; DB 2; Length 277;  
Matches 77; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 VIAGIRETEKFFYIVQEEKYRESLTHCRIRGMLAMPKDEAANTLIADYVAKSGFFRV 60

Db 148 VIAGIRETEKFFYIVQEEKYRESLTHCRIRGMLAMPKDEYVNTLIADYVAKSGFFRV 207

QY 61 FIGVNDLEREGQYMTDNT 80

Db 208 FIGVNDLEREGQYVTDNT 227

### RESULT 2

A37289

tetranectin homolog - reef shark

C:Species: Carcharhinus springeri (reef shark)

C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999

C:Accession: A37289; A37287

R:Neame, P.J.; Young, C.N.; Treep, J.T.

Protein Sci. 1, 161-168, 1992

A:Title: Primary structure of a protein isolated from reef shark Carcharhinus springeri

A:Reference number: A37289; MUID:93284081; PMID:1304877

A:Accession: A37289

A:Molecule type: Protein

A:Residues: 1-166 <NE2>

C:Superfamily: tetranectin; C-type lectin homology

C:Keywords: cartilage

F:37-160/Domain: C-type lectin homology <LCH>

F:37-47,64-160,136-152/disulfide bonds: #status predicted

Query Match 21.8%; Score 91; DB 1; Length 166;  
Best Local Similarity 28.8%; Pred. No. 0.0031;  
Matches 21; Conservative 15; Mismatches 35; Indels 2; Gaps 1;  
  
QY 10 EXFYVIVOEKNYRESLTHCRIRGMLAMPKDEAANTLIADYVAKS--GFPRVFIGVNDL 67  
DB 45 KCYLASGSKSYHAANEEDCTAAGGTLSPRSSDEGNSLSYAKSLVGDARDFWIGVNDM 104  
QY 68 EREGQYMTDNT 80  
DB 105 TTEGRFVDVNGLP 117  
  
RESULT 3  
HIV gp120-binding C-type lectin - human  
C/Species: Homo sapiens (man)  
C/Date: 21-Sep-1993 #sequence\_revision 18-Nov-1994 #text\_change 01-Dec-1995  
C/Accession: A46274  
R/Curtis, B.M.; Scharnowske, S.; Watson, A.J.  
Proc. Natl. Acad. Sci. U.S.A. 89, 8356-8360, 1992  
A/Title: Sequence and expression of a membrane-associated C-type lectin that exhibits CD  
A/Reference number: A46274; MUID:92390446; PMID:11518869  
A/Accession: A46274  
A/Status: preliminary  
A/Molecule type: nucleic acid  
A/Residues: 1-404 <CUR>  
A/Experimental source: placenta  
A/Note: sequence extracted from NCBI backbone (NCBIN:113134, NCBI:P:113135)  
C/Superfamily: C-type lectin homology  
F:256-377/Domain: C-type lectin homology <LCH>  
  
Query Match 21.2%; Score 88.5; DB 2; Length 404;  
Best Local Similarity 25.0%; Pred. No. 0.018;  
Matches 17; Conservative 20; Mismatches 30; Indels 1; Gaps 1;  
  
QY 13 YIVOEKNYRESLTHCRIRGMLAMPKDEAANTLIADYVAKSGFPRVFIGVNDLREQ 72  
DB 268 YFMSQNSQNHDSITACKVEGAQLWIKSAEQNFLOQSSRSNRP-TWMLGSLDNLQEGT 326  
QY 73 YNFTDNT 80  
DB 327 MQWVDGSP 334  
  
RESULT 4  
S33603  
surfactant protein D - bovine  
C/Species: Bos primigenius taurus (cattle)  
C/Date: 02-Dec-1993 #sequence\_revision 01-Sep-1995 #text\_change 17-Mar-1999  
C/Accession: S33603  
R/Lim, B.B.; Lu, J.; Reid, K.B.M.  
Immunology 78, 159-165, 1993  
A/Title: Structural similarity between bovine conglutinin and bovine lung surfactant pro  
A/Reference number: S33603; MUID:93170856; PMID:8436402  
A/Accession: S33603  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-369 <LIM>  
C/Superfamily: pulmonary surfactant protein D; C-type lectin homology  
F:248-367/Domain: C-type lectin homology <LCH>  
  
Query Match 20.0%; Score 83.5; DB 2; Length 369;  
Best Local Similarity 25.3%; Pred. No. 0.062;  
Matches 19; Conservative 16; Mismatches 39; Indels 1; Gaps 1;  
  
QY 6 RTESEKYYIVOEKNYRESLTHCRIRGMLAMPKDEAANTLIADYVAKSGFPRVFIGV 65  
DB 252 RSVGKEIKFTVGSXTFQDAQICTQAGGQLPSRSGAENEALQ-LATAQNKAFPLMS 310  
QY 66 DLREGQYMTDNT 80  
DB 311 DTRKEGTFTYPTGP 325

## RESULT 5

B56395  
secretory phospholipase A2 receptor precursor, soluble form - human  
C/Species: Homo sapiens (man)  
C/Date: 21-Jul-1995 #sequence\_revision 21-Jul-1995 #text\_change 21-Jan-2000  
C/Accession: B56395  
R/Ancian, P.; Lambeau, G.; Mattei, M.G.; Lazdunski, M.  
J. Biol. Chem. 270, 8963-8970, 1995  
A/Title: The human 180-kDa receptor for secretory phospholipases A-2. Molecular cloning,  
A/Reference number: A56395; MUID:95238395; PMID:7721806  
A/Accession: B56395  
A/Status: preliminary; not compared with conceptual translation  
A/Molecule type: mRNA  
A/Residues: 1-1328 <ANC>  
A/Cross-references: GB:U17034; NID:G862376; PIDN:AA50163.1; PID:G862377  
C/Genetics:  
A/Map position: 2q23-q24  
C/Superfamily: phospholipase A2 receptor; C-type lectin homology; fibronectin type II re  
C/Keywords: alternative splicing; extracellular protein  
F:180-221/Domain: fibronectin type II repeat homology <2F1>  
F:380-503/Domain: C-type lectin homology <LCH>

Query Match 19.8%; Score 82.5; DB 2; Length 1326;

Best Local Similarity 26.7%; Pred. No. 0.38;

Matches 16; Conservative 19; Mismatches 24; Indels 1; Gaps 1;

QY 21 NYRESLTHCRIRGMLAMPKDEAANTLIADYVAKSGFPRVFIGVNDLREQYMTDNT 80

DB 254 SWSEAHSSCOMGGTLLSITDETEENFIREHMS-SKTVEVWVGLNQLDDEAGWQSDGTP 312

## RESULT 6

A56395  
secretory phospholipase A2 receptor precursor, transmembrane form - human  
C/Species: Homo sapiens (man)  
C/Date: 21-Jul-1995 #sequence\_revision 21-Jul-1995 #text\_change 20-Aug-1999  
C/Accession: A56395  
R/Ancian, P.; Lambeau, G.; Mattei, M.G.; Lazdunski, M.  
J. Biol. Chem. 270, 8963-8970, 1995  
A/Title: The human 180-kDa receptor for secretory phospholipases A-2. Molecular cloning,  
A/Reference number: A56395; MUID:95238395; PMID:7721806  
A/Accession: A56395  
A/Status: preliminary; not compared with conceptual translation  
A/Molecule type: mRNA  
A/Residues: 1-1465 <ANC>  
A/Cross-references: GB:U17033; NID:G862374; PIDN:AAA70110.1; PID:G862375  
C/Genetics:  
A/Map position: 2q23-q24  
C/Superfamily: phospholipase A2 receptor; C-type lectin homology; fibronectin type II re  
C/Keywords: alternative splicing; transmembrane protein  
F:180-221/Domain: fibronectin type II repeat homology <2F1>  
F:380-503/Domain: C-type lectin homology <LCH>

Query Match 19.8%; Score 82.5; DB 2; Length 1465;

Best Local Similarity 26.7%; Pred. No. 0.43;

Matches 16; Conservative 19; Mismatches 24; Indels 1; Gaps 1;

QY 21 NYRESLTHCRIRGMLAMPKDEAANTLIADYVAKSGFPRVFIGVNDLREQYMTDNT 80

DB 254 SWSEAHSSCOMGGTLLSITDETEENFIREHMS-SKTVEVWVGLNQLDDEAGWQSDGTP 312

## RESULT 7

THUN  
tetranectin precursor [validated] - human  
N/Alternate names: plasminogen-kringle 4 binding protein  
C/Species: Homo sapiens (man)  
C/Date: 30-Jun-1992 #sequence\_revision 03-Aug-1995 #text\_change 08-Dec-2000  
A/Accession: S24126; A56835; A29747; I38359; S19865  
R/Berglund, L.; Petersen, T.E.  
FEBS Lett. 309, 15-19, 1992



A:Title: The gene structure of tetranectin, a plasminogen binding protein.  
A:Reference number: S24126; MUID:92380263; PMID:1511740  
A:Accession: S24126  
A:Molecule type: DNA  
A:Residues: 1-202 <BER>  
R:Wewer, U.M.; Albrechtsen, R.  
Lab. Invest. 67, 253-262, 1992  
A:Title: Tetranectin, a plasminogen kringle 4-binding protein. Cloning and gene expression.  
A:Reference number: A56835; MUID:92365345; PMID:1354271  
A:Accession: A56835  
A:Molecule type: mRNA  
A:Residues: 1-202 <WEW>  
A:Cross-references: EMBL:X70911  
A:Experimental source: placenta  
R:Fuhrdorff, J.; Clemensen, I.; Magnusson, S.  
Biochemistry 26, 6757-6764, 1987  
A:Title: Primary structure of tetranectin, a plasminogen kringle 4 binding plasma protein  
A:Reference number: A29747; MUID:88107595; PMID:3427041  
A:Accession: A29747  
A:Molecule type: protein  
A:Residues: 22-105, G, 107-202 <FUH>  
A:Experimental source: plasma  
A>Note: 55-Ser and 58-Met were also found  
C:Genetics:  
A:Gene: GDB:TNA  
A:Cross-references: GDB:135032; OMIM:187520  
A:Map position: 3p22-3p21.3  
A:Introns: 37/1; 70/1  
C:Complex: homotetramer  
C:Superfamily: tetranectin; C-type lectin homology  
C:Keywords: glycoprotein; plasma; tetramer  
F:1-21/Dominant: signal sequence #status predicted <SIG>  
F:22-202/Product: tetranectin #status experimental <MAT>  
F:71-197/Dominant: C-type lectin homology <LCH>  
F:75/binding site: carbohydrate (Thr) (covalent) #status experimental  
F:71-81, 98-197, 173-189/Disulfide bonds: #status experimental

Query Match 19.7%; Score 82; DB 1; Length 202;  
Best Local Similarity 25.8%; Pred. No. 0.045;  
Matches 17; Conservative 18; Mismatches 29; Indels 2; Gaps 1;

QY 11 KYIIVQEENKYNRESLTGCRIRGGMLAMPKDEAAANTLIADYVAKS--GPRFRVFIGVNDLE 68  
Db 80 KCFLAFTQTTFHEASEDCISRGGLTSPGTGSNDALYEYLRSVGNEAEIWGLINDMA 139  
QY 69 REGQYM 74  
Db 140 ASGTWV 145

RESULT 8  
Tt9259  
hypothetical protein C14A6.1 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
C:Accession: Tt9259  
R:Morimore, B.  
submitted to the EMBL Data Library, November 1996  
A:Reference number: Z19098  
A:Accession: Tt9259  
A>Status: preliminary; translated from GB/EMBL/DDBU  
A:Molecule type: DNA  
A:Residues: 1-321 <WI>  
A:Cross-references: EMBL:Z81470; PIDN:CA503881.1; GSPDB:GN00023; CBSP:C14A6.1  
A:Experimental source: clone C14A6  
C:Genetics:  
A:Gene: CBSP:C14A6.1  
A:Map position: 5  
A:Introns: 32/2; 164/1; 232/1

Query Match 19.7%; Score 82; DB 2; Length 321;  
Best Local Similarity 30.4%; Pred. No. 0.079;

MATCHES 21; Conservative 13; Mismatches 29; Indels 6; Gaps 2;  
QY 13 YIIIVQEENKYNRESLTGCRIRGGMLAMPKDEAAANTLI-----ADVVAKSGRFRVFIGVNDLE 68  
Db 36 YFTAPAFSFAEQ--QQNLGGHLASVQGQENALLQSNAANSFKNSYDIWIGANDLE 93  
QY 69 REGQYMF 77  
Db 94 TSGTWKMTD 102

RESULT 9  
A33570  
Collectin-43 - bovine  
N:Alternate names: lectin CL-43  
C:Species: Bos primigenius taurus (cattle)  
C>Date: 12-Apr-1995 #sequence\_revision 23-Feb-1996 #text\_change 17-Mar-1999  
A:Accession: A53570; A46689  
R:Lim, B.L.; Willis, A.C.; Reid, K.B.M.; Lu, J.; Laursen, S.B.; Jensenius, J.C.; Holmsk  
J. Biol. Chem. 269, 11820-11824, 1994  
A:Title: Primary structure of bovine collectin-43 (CL-43). Comparison with conglutinin.  
A:Reference number: A53570; MUID:94216283; PMID:8163480  
A:Accession: A53570  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-301 <LIM>  
A:Cross-references: GB:X75912  
R:Holmskov, U.; Teisner, B.; Willis, A.C.; Reid, K.B.; Jensenius, J.C.  
J. Biol. Chem. 268, 10120-10125, 1993  
A:Title: Purification and characterization of a bovine serum lectin (CL-43) with structu  
A:Reference number: A46689; MUID:93252891; PMID:8486682  
A:Accession: A46689  
A:Molecule type: protein  
A:Residues: 1-27 <HOH>  
A:Experimental source: serum  
A>Note: sequence extracted from NCBI backbone (NCBIP:131234)  
C:Superfamily: pulmonary surfactant protein D; C-type lectin homology  
C:Keywords: lectin  
F:177-299/Dominant: C-type lectin homology <LCH>

Query Match 19.5%; Score 81.5; DB 2; Length 301;  
Best Local Similarity 28.4%; Pred. No. 0.083;  
Matches 19; Conservative 15; Mismatches 30; Indels 3; Gaps 2;

QY 10 EKFYIVQEENKYNRESLTGCRIRGGMLAMPKDEAAANTLIADYV-AKSGFRFRVFIGVNDLE 68  
Db 185 EKIFKTAGVKYSYSDAEQLCREAKGOLASPRSAENEATVLRAKNK--HAYLSMNDIS 242  
QY 69 REGQYMF 75  
Db 243 KEKGFTY 249

RESULT 10  
A36563  
mannose receptor precursor - human  
C:Species: Homo sapiens (man)  
C>Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
A:Accession: A36563; A60926; A4255; B44255; C44255; F44255; F44255; G44255; H4;  
R:Taylor, M.E.; Conary, J.T.; Lennartz, M.R.; Stahl, P.D.; Drickamer, K.  
J. Biol. Chem. 265, 12156-12162, 1990  
A:Title: Primary structure of the mannose receptor contains multiple motifs resembling c  
A:Reference number: A36563; MUID:90324192; PMID:2373685  
A:Accession: A36563  
A:Molecule type: mRNA  
A:Residues: 1-1456 <TA>  
A:Cross-references: GB:J05550; NID:g188675; PIDN:AAA59868.1; PID:g188676  
A>Note: parts of this sequence, including the amino end of the mature protein, were conf  
R:Berkowitz, R.A.B.; Sastry, K.; Bailly, P.; Warner, A.  
J. Exp. Med. 172, 1785-1794, 1990  
A:Title: Molecular characterization of the human macrophage mannose receptor: demonstrat  
A:Reference number: A60926; MUID:91079783; PMID:2258707  
A:Accession: A60926

A>Status: nucleic acid sequence not shown  
A/Molecule type: mRNA  
A/Residues: 1-1333, T, 1335-1456 <EZE>  
A/Cross-references: GB:X55635  
A/Note: translation of the nucleotide sequence is incomplete  
R/Kit: in the authors' translation additional residues Pro-Glu-Ile are shown after 497-  
A/Name: S.J.; Ruiz, N.; Bezouska, K.; Drickamer, K.  
Genomics 14, 721-727, 1992  
A/Title: Organization of the gene encoding the human macrophage mannose receptor (MRC1).  
A/Reference number: A44255; MUID:93052405; PMID:1294118  
A/Accession: A44255  
A/Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra  
A/Molecule type: DNA  
A/Residues: 155-233, 'KSAL', 238-283;346-428;492-569;631-714,716-719;783-820,'N',822-865;  
A/Note: sequence extracted from NCBI backbone (NCBIP:118415, NCBIP:118421, NCBIP:118428,  
C/Genetics:  
A/Gene: GDB:MRC1  
A/Cross-references: GDB:133759; OMIM:153618  
A/Map position: 10p13-10p13  
C/Superfamily: phospholipase A2 receptor; C-type lectin homology; fibronectin type II re  
C/Keywords: duplication; lectin; tandem repeat; transmembrane protein  
F1-18/Domain: signal sequence #status predicted <SIG>  
F168-209/Domain: fibronectin type II repeat homology <2F1>  
F223-340/Domain: C-type lectin homology <LCH1>  
F362-486/Domain: C-type lectin homology <LCH2>  
F945-1079/Domain: C-type lectin homology <LCH3>  
  
Query Match 19.5%; Score 81.5; DB 1; Length 1456;  
Best Local Similarity 28.8%; Pred. No. 0.56;  
Matches 19; Conservative 15; Mismatches 31; Indels 1; Gaps 1;  
  
QY 12 FYIVQEKYKRESLTHCRIGGMLAMPKDEAANTLIADYVAKSGFRVPIGVNDLERSG 71  
DB 960 FGFMEERKNQWARKCIGFGNGLVSIONEKEQAFIT-YHMKDSTPSAWTGLNDVNSEH 1018  
QY 72 QYMFTD 77  
DB 1019 TELWTD 1024  
  
RESULT 11  
LNHUP6  
pulmonary surfactant protein A precursor (genomic clone) - human  
N/Alternate names: alveolar proteinosis protein; pulmonary surfactant 32K apoprotein; pu  
C/Species: Homo sapiens (man)  
C/Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 16-Jul-1999  
C/Accession: A24622; A43628  
R/White, R.T.; Damm, D.; Miller, J.; Spratt, K.; Schilling, J.; Hawgood, S.; Benson, B.  
Nature 317, 361-363, 1985  
A/Title: Isolation and characterization of the human pulmonary surfactant apoprotein gen  
A/Reference number: A24622; MUID:86014366; PMID:2995821  
A/Accession: A24622  
A/Molecule type: DNA  
A/Residues: 1-248 <WHI>  
A/Cross-references: GB:M30838; NID:G190564; PIDN:AAA36510.1; PID:G190565  
A/Note: the sequence in GenBank entry HUMPSAP, release 109.0, (PID:G190565) has the cod  
A/Note: four nucleotide differences, producing amino acid differences at positions 45, 5  
R/Haagman, H.P.; White, R.T.; Schilling, J.; Lau, K.; Benson, B.J.; Golden, J.; Hawgood  
Am. J. Physiol. 257, L421-L429, 1989  
A/Title: Studies of the structure of lung surfactant protein SP-A.  
A/Reference number: A43628; MUID:90119861; PMID:2610270  
A/Accession: A43628  
A/Molecule type: protein  
A/Residues: 143-150;220-240;243-248 <HAA>  
C/Residues: 143-150;220-240;243-248 <HAA>  
C/Species: Pulmonary surfactant is a complex of phospholipids and proteins that lowers t  
C/Comment: This protein is a sialoglycoprotein synthesized by alveolar type II cells. It  
pendent on the presence of calcium ions.  
C/Genetics:  
A/Gene: GDB:SFTPA1; SFTPL1; SP-A; SP-A1  
A/Cross-references: GDB:119593; OMIM:178630  
A/Map position: 10q22-10q23  
A/Introns: 58/1; 98/1; 124/1  
C/Superfamily: mannose-binding lectin; C-type lectin homology

C/Keywords: alveolar proteinosis; calcium; gaseous exchange; glycoprotein; hydroxylysine  
F1-20/Domain: signal sequence #status predicted <SIG>  
F121-248/Product: pulmonary surfactant protein A #status predicted <VAT>  
F128-100/Domain: collagenous #status predicted <COL>  
F127-246/Domain: C-type lectin homology <LCH>  
F306/Disulfide bonds: interchain #status experimental  
F30.33.36.42.57.63.76.79.82.91.97/Modified site: 4-hydroxyproline (Pro) #status predict  
F51.88/Modified site: 5-hydroxylysine (Lys) #status predicted  
F155-246.224-238/Diulfide bonds: #status experimental  
F1207/Binding site: carbohydrate (Asn) (covalent) #status predicted  
  
Query Match 18.8%; Score 78.5; DB 1; Length 248;  
Best Local Similarity 28.8%; Pred. No. 0.15;  
Matches 15; Conservative 13; Mismatches 23; Indels 1; Gaps 1;  
  
QY 29 CRIRGMLAMPKDEAANTLIADYVAKSGFRVPIGVNDLERSQYMFDTNTP 80  
DB 155 CARAGGRIAPRNPENEALASPVKKYNTY-AVVGITGSPGDFRISDGT 205  
  
RESULT 12  
LNHUP6  
pulmonary surfactant protein A precursor (clone 6A) - human  
N/Alternate names: pulmonary surfactant 32K apoprotein; pulmonary surfactant-associated  
C/Species: Homo sapiens (man)  
C/Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 16-Jul-1999  
C/Accession: A25720  
R/Floros, J.; Steinbrink, R.; Jacobs, K.; Phelps, D.; Kriz, R.; Recny, M.; Sultzman, L.;  
J. Biol. Chem. 261, 9029-9033, 1986  
A/Title: Isolation and characterization of cDNA clones for the 35-kDa pulmonary surfact  
A/Reference number: A25720; MUID:86250832; PMID:3755136  
A/Accession: A25720  
A/Molecule type: mRNA  
A/Residues: 1-248 <FLO>  
A/Cross-references: GB:M31686; NID:G190669; PIDN:AAA60211.1; PID:G190670  
A/Note: part of the sequence was confirmed by protein sequencing  
A/Note: the amino end of the mature protein, which was not identified, is partially acet  
A/Note: clones corresponding to two different proteins were sequenced. Cotranslational t  
C/Genetics:  
A/Gene: GDB:SFTPA1; SFTPL1; SP-A; SP-A1  
A/Cross-references: GDB:119593; OMIM:178630  
A/Map position: 10q22-10q23  
C/Superfamily: mannose-binding lectin; C-type lectin homology  
C/Keywords: acetylated amino end; alveolar proteinosis; calcium; gaseous exchange; glyc  
F1-20/Domain: signal sequence #status predicted <SIG>  
F121-248/Product: pulmonary surfactant protein A #status predicted <VAT>  
F127-246/Domain: C-type lectin homology <LCH>  
F121/Modified site: acetylated amino end (Glu) (in mature form) #status predicted  
F30.33.36.42.54.57.63.76.79.82.91.97/Modified site: 4-hydroxyproline (Pro) #status pre  
F1207/Binding site: carbohydrate (Asn) (covalent) #status predicted  
  
Query Match 18.8%; Score 78.5; DB 1; Length 248;  
Best Local Similarity 28.8%; Pred. No. 0.15;  
Matches 15; Conservative 13; Mismatches 23; Indels 1; Gaps 1;  
  
QY 29 CRIRGMLAMPKDEAANTLIADYVAKSGFRVPIGVNDLERSQYMFDTNTP 80  
DB 155 CARAGGRIAPRNPENEALASPVKKYNTY-AVVGITGSPGDFRISDGT 205  
  
RESULT 13  
LNHUP1  
pulmonary surfactant protein A precursor (clone 1A) - human  
N/Alternate names: pulmonary surfactant 32K apoprotein; pulmonary surfactant-associated  
C/Species: Homo sapiens (man)  
C/Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 16-Jul-1999  
C/Accession: B25720  
R/Floros, J.; Steinbrink, R.; Jacobs, K.; Phelps, D.; Kriz, R.; Recny, M.; Sultzman, L.;  
J. Biol. Chem. 261, 9029-9033, 1986  
A/Title: Isolation and characterization of cDNA clones for the 35-kDa pulmonary surfact  
A/Reference number: A25720; MUID:86250832; PMID:3755136  
A/Accession: B25720  
A/Molecule type: mRNA

A;Residues: 1-248 <FLO>  
A;Cross-references: GB:K03475  
A;Note: part of the sequence was confirmed by protein sequencing  
A;Note: the amino end of the mature protein, which was not identified, is partially acetylated  
A;Note: clones corresponding to two different proteins were sequenced. Cotranslational maturation  
C;Genetics:  
A;Gene: GDB:SFTPA1; SFTPL1; SP-A; SP-A1  
A;Cross-references: GDB:119593; OMIM:178630  
A;Map position: 10q22-10q23  
C;Superfamily: mannose-binding lectin; C-type lectin homology  
C;Keywords: acetylated amino end; alveolar proteinosis; calcium; gaseous exchange; glycosylation  
F;1-20/Domain: signal sequence #status predicted <SIG>  
F;21-248/Product: pulmonary surfactant protein A #status predicted <MAT>  
F;127-246/Domain: C-type lectin homology <LCH>  
F;21/Modified site: acetylated amino end (Glu) (in mature form) #status predicted  
F;30,33,36,42,54,57,63,76,82,91,97/Modified site: 4-hydroxyproline (Pro) #status predicted  
F;207/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 18.8%; Score 78.5; DB 1; Length 248;  
Best Local Similarity 28.8%; Pred. No. 0.15;  
Matches 15; Conservative 13; Mismatches 23; Indels 1; Gaps 1;

QY 29 CRIRGMLAMPKDEAANTLIADYVAKSGFFRVFVGNDLREGQYMFDTNTP 80  
Db 155 CARAGRIAPNPENEAIAAFVKKYNTY-AYVGLTEGSPGDFRYS DCTP 205

RESULT 14  
I51921  
pulmonary surfactant-associated protein A1 - human  
N;Alternate names: SP-A1  
C;Species: Homo sapiens (man)  
C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 20-Aug-1999  
C;Accession: I51921  
R;Katyay, S.I.; Singh, G.; Locker, J.  
A;Title: Characterization of a second human pulmonary surfactant-associated protein SP-A  
A;Reference number: I51921; MUID:92198680; PMID:1372511  
A;Accession: I51921  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-248 <RES>  
A;Cross-references: GB:M68519; NID:g338048; PIDN:AAA60319.1; PID:g338049  
C;Genetics:  
A;Gene: GDB:SFTPA1; SFTPL1; SP-A; SP-A1  
A;Cross-references: GDB:119593; OMIM:178630  
A;Map position: 10q22-10q23  
A;Introns: 58/1; 98/1; 124/1  
C;Superfamily: mannose-binding lectin; C-type lectin homology  
F;127-246/Domain: C-type lectin homology <LCH>

Query Match 18.8%; Score 78.5; DB 2; Length 248;  
Best Local Similarity 28.8%; Pred. No. 0.15;  
Matches 15; Conservative 13; Mismatches 23; Indels 1; Gaps 1;

QY 29 CRIRGMLAMPKDEAANTLIADYVAKSGFFRVFVGNDLREGQYMFDTNTP 80  
Db 155 CARAGRIAPNPENEAIAAFVKKYNTY-AYVGLTEGSPGDFRYS DCTP 205

RESULT 15  
JC4031  
tetranectin precursor - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 13-Jun-1995 #sequence\_revision 14-Jul-1995 #text\_change 20-Aug-1999  
C;Accession: JC4031  
R;Sorensen, C.B.; Berglund, L.; Petersen, T.E.  
Gene 152, 243-245, 1995  
A;Title: Cloning of a cDNA encoding murine tetranectin.  
A;Reference number: JC4031; MUID:95137396; PMID:7835708  
A;Accession: JC4031  
A;Molecule type: mRNA  
A;Residues: 1-202 <SOR>

A;Cross-references: EMBL:X79199; NID:g671561; PIDN:CAA55791.1; PID:g671562  
A;Experimental source: lung  
C;Comment: this protein binds plasminogen, and may play a role in invasive cancer.  
C;Superfamily: tetranectin; C-type lectin homology  
F;1-21/Domain: signal sequence #status predicted <SIG>  
F;22-202/Product: tetranectin #status predicted <MAT>  
F;71-197/Domain: C-type lectin homology <LCH>

Query Match 18.7%; Score 78; DB 2; Length 202;  
Best Local Similarity 27.1%; Pred. No. 0.13;  
Matches 16; Conservative 14; Mismatches 27; Indels 2; Gaps 1;

QY 18 BEKNYRESLTHCRIRGMLAMPKDEAANTLIADYVAKS--GFFRVFVGNDLREGQYM 74  
Db 87 QPKTFHEASEDCISQGGTGTGTPQSELENEALFVYARHSVGNDAIWLGLNDMAEGAWV 145

Search completed: March 8, 2004, 12:16:21  
Job time : 22.1454 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 8, 2004, 12:07:46 ; Search time 20.793 Seconds  
(without alignments)  
198.629 Million cell updates/sec

Title: US-09-600-932-2\_COPY\_148\_227

Perfect score: 417  
Sequence: 1 VIAGRETEKPYIVQSEK.....FIGVNDLEREQYMTDTP 80

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

#### Database :

Issued Patents AA:\*

- 1: /cgn2\_6/prodata/2/aaa/5A\_COMB.pep:\*
- 2: /cgn2\_6/prodata/2/aaa/5B\_COMB.pep:\*
- 3: /cgn2\_6/prodata/2/aaa/6A\_COMB.pep:\*
- 4: /cgn2\_6/prodata/2/aaa/6B\_COMB.pep:\*
- 5: /cgn2\_6/prodata/2/aaa/PCTUS\_COMB.pep:\*
- 6: /cgn2\_6/prodata/2/aaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	98.5	23.6	123	4	US-09-535-521-25
2	98.5	23.6	128	4	US-09-535-521-8
3	98.5	23.6	139	4	US-09-535-521-11
4	98.5	23.6	141	4	US-09-535-521-14
5	98.5	23.6	187	4	US-09-535-521-17
6	98.5	23.6	208	4	US-09-535-521-20
7	98.5	23.6	292	4	US-09-535-521-2
8	98.5	23.6	292	4	US-09-535-521-5
9	88.5	21.2	404	4	US-09-517-605-2
10	85	20.4	197	4	US-09-602-877A-99
11	82	19.7	202	1	US-08-469-486-56
12	82	19.7	202	1	US-08-469-658-56
13	81.5	19.5	1456	4	US-09-976-594-168
14	78	18.7	328	4	US-09-065-040-8
15	78	18.7	328	4	US-09-065-040-12
16	77.5	18.6	115	6	5514582-18
17	76.5	18.3	161	3	US-09-011-735-6
18	76.5	18.3	351	3	US-09-011-735-1
19	76.5	18.3	351	4	US-09-029-156-1
20	74.5	17.9	1479	3	US-08-840-062-2
21	74.5	17.9	1479	3	US-08-840-062-4
22	74	17.7	108	6	5514582-16
23	73	17.5	1722	4	US-09-194-612A-1
24	72.5	17.4	337	4	US-09-489-039A-13994
25	72	17.3	343	4	US-09-065-040-4
26	71.5	17.1	145	3	US-08-772-440-14
27	71.5	17.1	1487	3	US-08-840-062-7

28 71 17.0 107 6 5514582-17  
29 70.5 16.9 125 3 US-08-722-126A-7  
30 70.5 16.9 125 5 PCT-US95-04258-7  
31 70.5 16.9 287 1 US-08-365-103B-4  
32 70.5 16.9 300 1 US-08-365-103B-6  
33 70.5 16.9 327 1 US-08-365-103B-2  
34 69.5 16.7 110 6 5514582-9  
35 69.5 16.7 114 3 US-08-722-126A-6  
36 69.5 16.7 114 5 PCT-US95-04258-6  
37 69.5 16.7 188 3 US-08-722-126A-5  
38 69.5 16.7 188 5 PCT-US95-04258-5  
39 69.5 16.7 1463 1 US-08-220-603A-11  
40 68 16.3 1209 5 PCT-US95-04589-107  
41 68 16.3 1258 2 US-08-310-912A-107  
42 68 16.3 1258 3 US-09-301-085-107  
43 68 16.3 1294 3 US-08-930-996A-10  
44 67 16.1 131 3 US-08-772-440-23  
45 67 16.1 131 3 US-08-772-440-27

#### ALIGNMENTS

RESULT 1  
US-09-535-521-25  
; Sequence 25, Application US/09535521  
; Patent No. 6410714  
; GENERAL INFORMATION:  
; APPLICANT: Weber, Eric R.  
; TITLE OF INVENTION: NOVEL CANINE LOW AFFINITY IGE RECEPTOR (CANINE CD23)  
; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF  
; FILE REFERENCE: AL-5  
; CURRENT APPLICATION NUMBER: US/09/535,521  
; CURRENT FILING DATE: 2000-03-24  
; EARLIER APPLICATION NUMBER: 60/125,913  
; EARLIER FILING DATE: 1999-03-24  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 25  
; LENGTH: 123  
; TYPE: PRT  
; ORGANISM: Canis familiaris  
US-09-535-521-25

Query Match 23.6%; Score 98.5; DB 4; Length 123;  
Best Local Similarity 30.6%; Pred. No. 8.9e-06;  
Matches 22; Conservative 14; Mismatches 33; Indels 3; Gaps 1;  
QY 9 EKPYIVQEEKNVRESLTHORIGGMLAMPKDAANTLIADYVAKSGFFRVFIGVNDLE 68  
DB 14 QRKCYFGEPEPKMIOAFACSKLQGLASIHSEQEDFLARYANKKG---TWIGRLDLD 70  
QY 69 REGQYMTDTP 80  
DB 71 REGEFINDENP 82

RESULT 2  
US-09-535-521-8  
; Sequence 8, Application US/09535521  
; Patent No. 6410714  
; GENERAL INFORMATION:  
; APPLICANT: Weber, Eric R.  
; TITLE OF INVENTION: NOVEL CANINE LOW AFFINITY IGE RECEPTOR (CANINE CD23)  
; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF  
; FILE REFERENCE: AL-5  
; CURRENT APPLICATION NUMBER: US/09/535,521  
; CURRENT FILING DATE: 2000-03-24  
; EARLIER APPLICATION NUMBER: 60/125,913  
; EARLIER FILING DATE: 1999-03-24  
; NUMBER OF SEQ ID NOS: 26

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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Canis familiaris
US-09-535-521-8

Query Match      23.6%; Score 98.5; DB 4; Length 128;
Best Local Similarity 30.6%; Pred. No. 1.1e-06;
Matches 22; Conservative 14; Mismatches 33; Indels 3; Gaps 1;

QY 9 BEKFYIVQEKNYRESLTHCRIRGMLAMPKDEAANTLIADYVAKSGFFRVFIGVNDLE 68
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 11 QKCYTFGEPEPKWQIARFACSKLQGRLASIHSQEEDFLARYANKKG---TWIGLRDLD 67

QY 69 REGQYMTDNT 80
   |||:|||||:
Db 68 REGEFIWMDENP 79

RESULT 3
US-09-535-521-11
; Sequence 11, Application US/09535521
; Patent No. 6410714
; GENERAL INFORMATION:
; APPLICANT: Weber, Eric R.
; APPLICANT: McCall, Catherine A.
; TITLE OF INVENTION: NOVEL CANINE LOW AFFINITY IGE RECEPTOR (CANINE CD23)
; FILE REFERENCE: AL-5
; CURRENT APPLICATION NUMBER: US/09/535,521
; CURRENT FILING DATE: 2000-03-24
; EARLIER APPLICATION NUMBER: 60/125,913
; EARLIER FILING DATE: 1999-03-24
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 139
; TYPE: PRT
; ORGANISM: Canis familiaris
US-09-535-521-11

Query Match      23.6%; Score 98.5; DB 4; Length 139;
Best Local Similarity 30.6%; Pred. No. 1.1e-05;
Matches 22; Conservative 14; Mismatches 33; Indels 3; Gaps 1;

QY 9 BEKFYIVQEKNYRESLTHCRIRGMLAMPKDEAANTLIADYVAKSGFFRVFIGVNDLE 68
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 22 QKCYTFGEPEPKWQIARFACSKLQGRLASIHSQEEDFLARYANKKG---TWIGLRDLD 78

QY 69 REGQYMTDNT 80
   |||:|||||:
Db 79 REGEFIWMDENP 90

RESULT 4
US-09-535-521-14
; Sequence 14, Application US/09535521
; Patent No. 6410714
; GENERAL INFORMATION:
; APPLICANT: Weber, Eric R.
; APPLICANT: McCall, Catherine A.
; TITLE OF INVENTION: NOVEL CANINE LOW AFFINITY IGE RECEPTOR (CANINE CD23)
; FILE REFERENCE: AL-5
; CURRENT APPLICATION NUMBER: US/09/535,521
; CURRENT FILING DATE: 2000-03-24
; EARLIER APPLICATION NUMBER: 60/125,913
; EARLIER FILING DATE: 1999-03-24
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 141
; TYPE: PRT
; ORGANISM: Canis familiaris
US-09-535-521-14

Query Match      23.6%; Score 98.5; DB 4; Length 141;
Best Local Similarity 30.6%; Pred. No. 1.1e-05;
Matches 22; Conservative 14; Mismatches 33; Indels 3; Gaps 1;

QY 9 BEKFYIVQEKNYRESLTHCRIRGMLAMPKDEAANTLIADYVAKSGFFRVFIGVNDLE 68
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 24 QKCYTFGEPEPKWQIARFACSKLQGRLASIHSQEEDFLARYANKKG---TWIGLRDLD 80

QY 69 REGQYMTDNT 80
   |||:|||||:
Db 81 REGEFIWMDENP 92

RESULT 5
US-09-535-521-17
; Sequence 17, Application US/09535521
; Patent No. 6410714
; GENERAL INFORMATION:
; APPLICANT: Weber, Eric R.
; APPLICANT: McCall, Catherine A.
; TITLE OF INVENTION: NOVEL CANINE LOW AFFINITY IGE RECEPTOR (CANINE CD23)
; FILE REFERENCE: AL-5
; CURRENT APPLICATION NUMBER: US/09/535,521
; CURRENT FILING DATE: 2000-03-24
; EARLIER APPLICATION NUMBER: 60/125,913
; EARLIER FILING DATE: 1999-03-24
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 187
; TYPE: PRT
; ORGANISM: Canis familiaris
US-09-535-521-17

Query Match      23.6%; Score 98.5; DB 4; Length 187;
Best Local Similarity 30.6%; Pred. No. 1.1e-05;
Matches 22; Conservative 14; Mismatches 33; Indels 3; Gaps 1;

QY 9 BEKFYIVQEKNYRESLTHCRIRGMLAMPKDEAANTLIADYVAKSGFFRVFIGVNDLE 68
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 70 QKCYTFGEPEPKWQIARFACSKLQGRLASIHSQEEDFLARYANKKG---TWIGLRDLD 126

QY 69 REGQYMTDNT 80
   |||:|||||:
Db 127 REGEFIWMDENP 138

RESULT 6
US-09-535-521-20
; Sequence 20, Application US/09535521
; Patent No. 6410714
; GENERAL INFORMATION:
; APPLICANT: Weber, Eric R.
; APPLICANT: McCall, Catherine A.
; TITLE OF INVENTION: NOVEL CANINE LOW AFFINITY IGE RECEPTOR (CANINE CD23)
; FILE REFERENCE: AL-5
; CURRENT APPLICATION NUMBER: US/09/535,521
; CURRENT FILING DATE: 2000-03-24
; EARLIER APPLICATION NUMBER: 60/125,913
; EARLIER FILING DATE: 1999-03-24
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Canis familiaris
US-09-535-521-20
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; LENGTH: 1456
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673549 1674368CD1
US-09-976-594-168

Query Match
Best Local Similarity 19.5%; Score 81.5; DB 4; Length 1456;
Matches 19; Conservative 15; Mismatches 31; Indels 1; Gaps 1;

QY 12 FYIVQEKYRESLTHCRIRGGMLAMPKDEAAANTLIADYVAKSGFRVFGVNDLEREG 71
Db 960 FQFMEERQWQEQAKACIGFQGNLVLSIQNEKEQAFIT-YHKDSTFSAWTGLNDVNSEH 1018
QY 72 QYMTD 77
Db 1019 TFLWTD 1024

RESULT 14
US-09-065-040-8
; Sequence 8, Application US/09065040
; Patent No. 6541217
; GENERAL INFORMATION:
; APPLICANT: Hiraoka, Atsunobu
; APPLICANT: Sugimura, Atsushi
; APPLICANT: Mio, Hiroyuki
; TITLE OF INVENTION: HEMATOPOIETIC STEM CELL GROWTH FACTOR
; TITLE OF INVENTION:
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT &
; ADDRESSEE: DUNNER, LLP
; STREET: 1300 I Street, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/065,040
; FILING DATE: 27-APR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 087242/1997
; FILING DATE: 27-AUG-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP97/02349
; FILING DATE: 07-JUL-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Fordis, Jean B.
; REGISTRATION NUMBER: 32,984
; REFERENCE/DOCKET NUMBER: 04853.0026-00000
; TELEPHONE: 202-408-4400
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 328 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-065-040-8

Query Match
Best Local Similarity 18.7%; Score 78; DB 4; Length 328;
Matches 21; Conservative 19; Mismatches 33; Indels 4; Gaps 3;

QY 2 IAGIRETEEKFYIVQBEKNYRESLTHCRIRGGMLAMPKDEAAANTLIADYV--AKSGF-P 58
Db 183 LKGLR-LGHKCFILSRDFETQAAAQARCKARGGSLAQPADRQMDALSRYLRAALAPYNW 241
QY 59 RVFIGVNDLEREGQYMF 75
Db 242 PVLGVHDDRSEGLYLF 258

Query Match
Best Local Similarity 18.7%; Score 78; DB 4; Length 328;
Matches 21; Conservative 19; Mismatches 33; Indels 4; Gaps 3;

QY 2 IAGIRETEEKFYIVQBEKNYRESLTHCRIRGGMLAMPKDEAAANTLIADYV--AKSGF-P 58
Db 183 LKGLR-LGHKCFILSRDFETQAAAQARCKARGGSLAQPADRQMDALSRYLRAALAPYNW 241
QY 59 RVFIGVNDLEREGQYMF 75
Db 242 PVLGVHDDRSEGLYLF 258

RESULT 15
US-09-065-040-12
; Sequence 12, Application US/09065040
; Patent No. 6541217
; GENERAL INFORMATION:
; APPLICANT: Hiraoka, Atsunobu
; APPLICANT: Sugimura, Atsushi
; APPLICANT: Mio, Hiroyuki
; TITLE OF INVENTION: HEMATOPOIETIC STEM CELL GROWTH FACTOR
; TITLE OF INVENTION:
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT &
; ADDRESSEE: DUNNER, LLP
; STREET: 1300 I Street, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/065,040
; FILING DATE: 27-APR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 262252/1996
; FILING DATE: 27-AUG-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 087242/1997
; FILING DATE: 24-MAR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP97/02349
; FILING DATE: 07-JUL-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Fordis, Jean B.
; REGISTRATION NUMBER: 32,984
; REFERENCE/DOCKET NUMBER: 04853.0026-00000
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 328 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-065-040-12

Query Match
Best Local Similarity 18.7%; Score 78; DB 4; Length 328;
Matches 21; Conservative 19; Mismatches 33; Indels 4; Gaps 3;

QY 2 IAGIRETEEKFYIVQBEKNYRESLTHCRIRGGMLAMPKDEAAANTLIADYV--AKSGF-P 58
Db 183 LKGLR-LGHKCFILSRDFETQAAAQARCKARGGSLAQPADRQMDALSRYLRAALAPYNW 241
QY 59 RVFIGVNDLEREGQYMF 75
Db 242 PVLGVHDDRSEGLYLF 258
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Db 242 PVLGVHRRSEGLYLF 258

Search completed: March 8, 2004, 12:17:28  
Job time : 20.793 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model  
Run on: March 8, 2004, 11:54:00 ; Search time 73.6564 Seconds  
(without alignments)  
306.882 Million cell updates/sec

Title: US-09-600-932-2\_COPY\_148\_227  
Perfect score: 417  
Sequence: 1 VIAGIRETEREFYIVQEK.....FIGVNDLEREGQYMTDNTP 80

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A.Geneseq\_25Jan04.\*  
1: geneseqp1980s.\*  
2: geneseqp1990s.\*  
3: geneseqp2000s.\*  
4: geneseqp2001s.\*  
5: geneseqp2002s.\*  
6: geneseqp2003as.\*  
7: geneseqp2003bs.\*  
8: geneseqp2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	417	100.0	159	5	ABBS6404 Human col
2	417	100.0	277	2	AAV25518 Human col
3	409	98.1	277	2	AAV41698 Human PRO
4	409	98.1	277	3	ABR44254 Human PRO
5	409	98.1	277	4	AAU29073 Human PRO
6	409	98.1	277	6	ABU58449 Human PRO
7	409	98.1	277	6	ABU87997 Novel hum
8	409	98.1	277	6	ABU84312 Human sec
9	409	98.1	277	6	ABR66186 Human sec
10	409	98.1	277	6	ABR65576 Human sec
11	409	98.1	277	6	ABU93516 Human sec
12	409	98.1	277	6	ABU82755 Human PRO
13	409	98.1	277	6	ABU89876 Novel hum
14	409	98.1	277	6	ABR68125 Human sec
15	409	98.1	277	6	ABU96178 Novel hum
16	409	98.1	277	6	ABU92609 Human sec
17	409	98.1	277	6	ABO08686 Human sec
18	409	98.1	277	6	ABO02738 Human sec
19	409	98.1	277	6	ABR74892 Human sec
20	409	98.1	277	6	ABR94654 Human sec
21	409	98.1	277	6	ABO25200 Novel hum
22	409	98.1	277	6	ABU85627 Human PRO
23	409	98.1	277	6	ABU98787 Novel hum
24	409	98.1	277	6	ABU98002 Novel hum
25	409	98.1	277	6	ABU91708 Novel hum

26	409	98.1	277	6	ABU72206 Novel hum
27	409	98.1	277	6	ABU89401 Human PRO
28	409	98.1	277	6	ABU86242 Human sec
29	409	98.1	277	6	ABU67455 Human PRO
30	409	98.1	277	6	ABU80483 Human PRO
31	409	98.1	277	6	ABR99401 Human sec
32	409	98.1	277	6	ABR98791 Human sec
33	409	98.1	277	6	ABO16314 Human sec
34	409	98.1	277	6	ABR92214 Human sec
35	409	98.1	277	6	ABO18855 Human sec
36	409	98.1	277	6	ABR78276 Human sec
37	409	98.1	277	6	ABU85012 Novel hum
38	409	98.1	277	6	ABO00151 Novel hum
39	409	98.1	277	6	ABO11483 Human sec
40	409	98.1	277	6	ABO02128 Human sec
41	409	98.1	277	6	ABU86702 Novel hum
42	409	98.1	277	6	ABU83397 Human sec
43	409	98.1	277	6	ABO06198 Novel hum
44	409	98.1	277	6	ABR59234 Human sec
45	409	98.1	277	6	ABO09296 Human sec

ALIGNMENTS

RESULT 1  
ABBS6404  
ID ABBS6404 standard; peptide; 159 AA.

XX AC ABBS6404;  
XX DT 19-FEB-2002 (first entry)  
XX DE Human collectin polypeptide SEQ ID NO 52.  
XX KW Human; collectin; CL-L2-1; CL-L2-2; mouse; antibacterial; virucide;  
XX KW protein therapy; infection; ds.  
XX OS Homo sapiens.  
XX PN WO200181401-A1.  
XX PD 01-NOV-2001.  
XX PF 23-APR-2001; 2001WO-JP003468.  
XX PR 21-APR-2000; 2000JP-00120358.  
XX PS (FUSO ) FUSO PHARM IND LTD.  
XX PI Wakamiya N, Keshi H, Ontani K, Sakamoto T, Kishi Y;  
XX DR WPI; 2002-055345/07.

XX PT New collectin family proteins, designated CL-L2-1 and CL-L2-2, expressed in kidney and for treatment and prevention of bacterial and viral infections.  
XX PT in kidney and for treatment and prevention of bacterial and viral infections.  
XX PS Claim 8; Page 68; 134pp; Japanese.  
XX CC The invention relates to human collectin family proteins (CL-L2-1 and CL-L2-2, sequences given in the specification, ABBS6407-ABBS6411 and CC ABBS6414-ABBS6416), their derivatives and fragments and a related CC collectin (CL-L2) of mouse origin (ABBS6412) and polynucleotides encoding CC all or part of the proteins. The proteins have antibacterial and virucide CC activity and are used for protein therapy and treatment, prevention and CC diagnosis of bacterial and viral infections. The present sequence is that CC of a collectin polynucleotide of the invention

XX SQ Sequence 159 AA;

Query Match 100.0%; Score 417; DB 5; Length 159;  
Best Local Similarity 100.0%; Pred. No. 4.5e-47;

Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VIAGIRETEEFYIVQBEKNYRESLTHCRIRGGLAMPKDEAANTLIADYVAKSGFFRV 60  
 DB 30 VIAGIRETEEFYIVQBEKNYRESLTHCRIRGGLAMPKDEAANTLIADYVAKSGFFRV 89

QY 61 FIGVNDLEREGQWFTDNT 80  
 DB 90 FIGVNDLEREGQWFTDNT 109

RESULT 2  
 AAY25518  
 ID AAY25518 standard; protein; 277 AA.  
 XX  
 AC AAY25518;  
 XX  
 DT 30-SEP-1999 (first entry)  
 XX  
 DE Human collectin protein.  
 XX  
 KW Collectin; human; antibacterial; antiviral; treatment; infection.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9937767-A1.  
 XX  
 PD 29-JUL-1999.  
 XX  
 PF 24-JUL-1998; 98WO-JP003328.  
 XX  
 PR 23-JAN-1998; 98JP-00011281.  
 XX  
 PA (FUSO ) FUSO PHARM IND LTD.  
 XX  
 PI Wakamiya N;  
 XX  
 DR WPI; 1999-458691/38.  
 XX  
 DR N-PSDB; AAX88323.  
 XX  
 PT New collectin protein of human origin and DNA encoding it.  
 XX  
 PS Claim 1; Page 42-44; 58pp; Japanese.  
 XX  
 CC This invention describes the isolation and characterisation of a novel  
 CC human collectin protein and its encoding polynucleotide. The human  
 CC collectin exhibits antibacterial and antiviral activity and can be used  
 CC as an agent for the treatment of human bacterial and viral infections.  
 CC This sequence represents the novel human collectin  
 XX  
 SQ Sequence 277 AA;

Query Match 100.0%; Score 417; DB 2; Length 277;  
 Best Local Similarity 100.0%; Pred. No. 9.8e-47;  
 Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VIAGIRETEEFYIVQBEKNYRESLTHCRIRGGLAMPKDEAANTLIADYVAKSGFFRV 60  
 DB 148 VIAGIRETEEFYIVQBEKNYRESLTHCRIRGGLAMPKDEAANTLIADYVAKSGFFRV 207

QY 61 FIGVNDLEREGQWFTDNT 80  
 DB 208 FIGVNDLEREGQWFTDNT 227

RESULT 3  
 AAY41698  
 ID AAY41698 standard; protein; 277 AA.  
 XX  
 AC AAY41698;  
 XX  
 DT 07-DEC-1999 (first entry)  
 XX

DE Human PRO702 protein sequence.  
 XX  
 KW Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;  
 KW probe; blood coagulation disorder; cancer; cellular adhesion disorder;  
 KW secreted protein; transmembrane protein.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9946281-A2.  
 XX  
 PD 16-SEP-1999.  
 XX  
 PF 08-MAR-1999; 99WO-US005028.  
 XX  
 PR 10-MAR-1998; 98US-0077450P.  
 PR 11-MAR-1998; 98US-0077632P.  
 PR 11-MAR-1998; 98US-0077641P.  
 PR 11-MAR-1998; 98US-0077649P.  
 PR 12-MAR-1998; 98US-007791P.  
 PR 13-MAR-1998; 98US-0078004P.  
 PR 17-MAR-1998; 98US-00040220.  
 PR 20-MAR-1998; 98US-0078886P.  
 PR 20-MAR-1998; 98US-0078910P.  
 PR 20-MAR-1998; 98US-0078936P.  
 PR 20-MAR-1998; 98US-0078939P.  
 PR 25-MAR-1998; 98US-0079294P.  
 PR 26-MAR-1998; 98US-0079656P.  
 PR 27-MAR-1998; 98US-0079663P.  
 PR 27-MAR-1998; 98US-0079664P.  
 PR 27-MAR-1998; 98US-0079689P.  
 PR 27-MAR-1998; 98US-0079728P.  
 PR 27-MAR-1998; 98US-0079786P.  
 PR 30-MAR-1998; 98US-0079920P.  
 PR 31-MAR-1998; 98US-0079923P.  
 PR 31-MAR-1998; 98US-0080105P.  
 PR 31-MAR-1998; 98US-0080107P.  
 PR 31-MAR-1998; 98US-0080165P.  
 PR 31-MAR-1998; 98US-0080194P.  
 PR 01-APR-1998; 98US-0080327P.  
 PR 01-APR-1998; 98US-0080328P.  
 PR 01-APR-1998; 98US-0080333P.  
 PR 01-APR-1998; 98US-0080334P.  
 PR 08-APR-1998; 98US-0081049P.  
 PR 08-APR-1998; 98US-0081070P.  
 PR 08-APR-1998; 98US-0081071P.  
 PR 09-APR-1998; 98US-0081135P.  
 PR 09-APR-1998; 98US-0081203P.  
 PR 09-APR-1998; 98US-0081229P.  
 PR 15-APR-1998; 98US-0081817P.  
 PR 15-APR-1998; 98US-0081838P.  
 PR 15-APR-1998; 98US-0081952P.  
 PR 15-APR-1998; 98US-0081955P.  
 PR 21-APR-1998; 98US-0082568P.  
 PR 21-APR-1998; 98US-0082569P.  
 PR 22-APR-1998; 98US-0082700P.  
 PR 22-APR-1998; 98US-0082704P.  
 PR 22-APR-1998; 98US-0082804P.  
 PR 23-APR-1998; 98US-0082767P.  
 PR 23-APR-1998; 98US-0082796P.  
 PR 27-APR-1998; 98US-008336P.  
 PR 28-APR-1998; 98US-0083322P.  
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 PR 29-APR-1998; 98US-0083554P.  
 PR 29-APR-1998; 98US-0083558P.  
 PR 29-APR-1998; 98US-0083559P.  
 PR 30-APR-1998; 98US-0083742P.  
 PR 05-MAY-1998; 98US-0084366P.  
 PR 06-MAY-1998; 98US-0084414P.

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PR 06-MAY-1998; 98US-0084441P.
PR 07-MAY-1998; 98US-0084598P.
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PR 30-JUL-1998; 98US-0094651P.
PR 11-SEP-1998; 98US-0100038P.
XX
XX (GETH ) GENENTECH INC.
PA
XX Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;
XX WPI; 1999-551358/46.
XX N-PSDB; AA233973.
XX
XX New secreted and transmembrane polypeptides and their polynucleotides,
XX useful for treating blood coagulation disorders, cancers and cellular
XX adhesion disorders.
XX
XX Claim 12; Fig 37; 530pp; English.
XX
XX The present invention describes secreted and transmembrane polypeptides
XX and their polynucleotides. The nucleotide sequences are useful as sources
XX of probes, primers, for chromosome mapping, and for generation of
XX antisense sequences. They can also be used to create transgenic animals.
XX The proteins can be used to treat a variety of diseases and disorders,
XX depending on their function. Diseases that may be treated include blood
XX coagulation disorders, cancers and cellular adhesion disorders. They may
XX also be used to raise antibodies. AA233891 to AA23438, and AA41685 to
XX AA41774 represent polynucleotide and polypeptide sequence given in the
XX exemplification of the present invention
XX
XX Sequence 277 AA;
XX
XX Query Match 98.1%; Score 409; DB 2; Length 277;
XX Best Local Similarity 98.8%; Pred. No. 1.1e-45;
XX Matches 79; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1 VIAGIRETEKFFYIVQEKYRESLTHCRIRGGMLAMPKDEAANTLIADYVAKSGFFRV 60
XX
XX 148 VIAGIRETEKFFYIVQEKYRESLTHCRIRGGMLAMPKDEAANTLIADYVAKSGFFRV 207
XX
XX 61 FIGVNDLREGQYMTDNT 80
XX
XX 208 FIGVNDLREGQYMTDNT 227
XX
XX RESULT 4
XX AAB44254
XX ID AAB44254 standard; protein; 277 AA.
XX

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AC AAB44254;
XX
XX 08-FEB-2001 (first entry)
XX
XX Human PRO702 (UNQ366) protein sequence SEQ ID NO:97.
XX
XX Human; secreted protein; transmembrane protein; PRO; EST; cytotstatic;
XX expressed sequence tag; detection; cancer.
XX
XX Homo sapiens.
XX
XX WO2000053755-A2.
XX
XX 14-SEP-2000.
XX
XX 18-FEB-2000; 2000WO-US004341.
XX
XX 08-MAR-1999; 99WO-US005028.
XX 12-MAR-1999; 99US-0123957P.
XX 29-MAR-1999; 99US-0126773P.
XX 21-APR-1999; 99US-0130232P.
XX 28-APR-1999; 99US-0131445P.
XX 14-MAY-1999; 99US-0134287P.
XX 23-JUN-1999; 99US-0141037P.
XX 26-JUL-1999; 99US-0145698P.
XX 29-OCT-1999; 99US-0162506P.
XX 30-NOV-1999; 99WO-US028213.
XX 02-DEC-1999; 99WO-US028551.
XX 16-DEC-1999; 99WO-US028565.
XX 30-DEC-1999; 99WO-US031243.
XX 30-DEC-1999; 99WO-US031274.
XX 05-JAN-2000; 2000WO-US000219.
XX 06-JAN-2000; 2000WO-US000277.
XX 06-JAN-2000; 2000WO-US000376.
XX
XX (GETH ) GENENTECH INC.
XX
XX Ashkenazi AJ, Baker KP, Botstein D, Desnovers L, Eaton DL;
XX Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
XX Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hallan KJ;
XX Kljavin IV, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
XX Stewart TA, Tamas D, Williams PM, Wood WI;
XX
XX WPI; 2000-611443/58.
XX N-PSDB; AAC78480.
XX
XX Novel PRO polypeptides and polynucleotides used in detection methods, to
XX target bioactive molecules to specific cells, and to modulate cellular
XX activities.
XX
XX Claim 12; Fig 37; 636pp; English.
XX
XX AAC78458 to AAC78599 represent polynucleotide and EST (expressed sequence
XX tag) sequences which encode secreted or transmembrane PRO polypeptides.
XX The PRO polynucleotides and polypeptides have cytostatic activity. The
XX polynucleotides and polypeptides can be used for detecting the presence
XX of PRO polypeptides in samples, for linking bioactive molecules to cells
XX and for modulating biological activities of cells, using the polypeptides
XX for specific targeting. The polypeptide targeting can be used to kill the
XX target cells, e.g. for the treatment of cancers. The polypeptide pairs
XX provide specific targeting of bioactive molecules to cells. AAC78600 to
XX AAC78987 represent PCR primers and probes used in the isolation of the
XX PRO polynucleotide sequences
XX
XX Sequence 277 AA;
XX
XX Query Match 98.1%; Score 409; DB 3; Length 277;
XX Best Local Similarity 98.8%; Pred. No. 1.1e-45;
XX Matches 79; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1 VIAGIRETEKFFYIVQEKYRESLTHCRIRGGMLAMPKDEAANTLIADYVAKSGFFRV 60
XX

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Db 148 VIAGIRETEKFFYIVQEEKNYRESLTHCRIRGGMLAMPKDEAANTLIADYVAKSGFFRV 207  
QY 61 FIGVNDLEREGQYMTDNT 80  
|||||  
Db 208 FIGVNDLEREGQYMTDNT 227  
|||||  
RESULT 5  
AAU29073  
ID AAU29073 standard; protein; 277 AA.  
XX AAU29073;  
AC  
XX  
DT 18-DEC-2001 (first entry)  
XX  
DE Human PRO polypeptide sequence #50.  
XX  
KW PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;  
KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;  
KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;  
KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.  
XX  
OS Homo sapiens.  
XX  
PN WO200168848-A2.  
XX  
PD 20-SEP-2001.  
XX  
PF 28-FEB-2001; 2001WO-US006520.  
XX  
PR 01-MAR-2000; 2000WO-US005601.  
PR 02-MAR-2000; 2000WO-US005841.  
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PR 21-MAR-2000; 2000US-0191048P.  
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PR 30-MAR-2000; 2000WO-US008439.  
PR 04-APR-2000; 2000US-0194449P.  
PR 04-APR-2000; 2000US-0194647P.  
PR 11-APR-2000; 2000US-0195975P.  
PR 11-APR-2000; 2000US-0196000P.  
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PR 22-MAY-2000; 2000WO-US014042.  
PR 30-MAY-2000; 2000WO-US014941.  
PR 02-JUN-2000; 2000WO-US015264.  
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PR 28-JUL-2000; 2000WO-US020710.  
PR 22-AUG-2000; 2000US-00644848.  
PR 24-AUG-2000; 2000WO-US023328.  
PR 08-NOV-2000; 2000WO-US030952.  
PR 01-DEC-2000; 2000WO-US032678.  
PR 20-DEC-2000; 2000WO-US034956.  
XX  
XX (GETH ) GENENTECH INC.  
PA Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;  
PI

PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;  
XX  
XX WPI; 2001-602746/68.  
DR N-PSDB; AAS45974.  
XX  
XX Novel nucleic acids encoding PRO polypeptides, used to diagnose the  
PT presence of tumors, such as prostate and breast tumors, in mammals and to  
PT screen for modulators of the compounds.  
XX  
XX Claim 11; Fig 100; 774pp; English.  
XX  
XX Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.  
CC The PRO polypeptides and their associated nucleic acids can be used to  
CC detect the presence of a tumour in a mammal by comparing the level of  
CC expression of a PRO polypeptide in a test sample of cells from the animal  
CC and a control sample of normal cells, whereby a higher level of  
CC expression in the test sample indicates the presence of a tumour in the  
CC mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats  
CC and rabbits but are preferably human. The polypeptides can be used to  
CC stimulate tumour necrosis factor (TNF) alpha release from human blood,  
CC when contacted with it. A specific polypeptide can be used to stimulate  
CC the proliferation or differentiation of chondrocyte cells. The PRO  
CC proteins can be used to determine the presence of tumours and also  
CC susceptibility to tumour development, particularly adrenal, lung, colon,  
CC breast, prostate, rectal, cervical, or liver tumours, in mammalian  
CC subjects. The oligonucleotide probes specific for the PRO nucleic acids  
CC can be used for genetic analysis of individuals with genetic disorders  
XX  
XX Sequence 277 AA;  
SQ  
Query Match 98.1%; Score 409; DB 4; Length 277;  
Best Local Similarity 98.8%; Pred. No. 1.le-45;  
Matches 79; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
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Db 148 VIAGIRETEKFFYIVQEEKNYRESLTHCRIRGGMLAMPKDEAANTLIADYVAKSGFFRV 207  
|||||  
QY 61 FIGVNDLEREGQYMTDNT 80  
|||||  
Db 208 FIGVNDLEREGQYMTDNT 227  
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RESULT 6  
ABU58449  
ID ABU58449 standard; protein; 277 AA.  
XX  
XX ABU58449;  
XX  
DT 15-APR-2003 (first entry)  
XX  
DE Human PRO polypeptide #50.  
XX  
KW Human; PRO; cytostatic; tumour; cancer; breast; lung; stomach; liver;  
KW dog; cat; cow; horse; sheep; pig; goat; rabbit; ADEPT;  
KW ant.body-dependent enzyme mediated prodrug therapy.  
XX  
XX Homo sapiens.  
XX  
XX US2003027272-A1.  
XX  
PD 06-FEB-2003.  
XX  
PF 21-JUN-2002; 2002US-00176492.  
XX  
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PR 29-OCT-1997; 97US-0063734P.  
PR 31-OCT-1997; 97US-0063870P.  
PR 31-OCT-1997; 97US-0064103P.  
PR 13-NOV-1997; 97US-0065311P.  
PR 21-NOV-1997; 97US-0066120P.  
PR 24-NOV-1997; 97US-0066466P.  
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PR 06-MAY-1998; 98US-0083366P.  
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Query Match 98.1%; Score 409; DB 6; Length 277;
Best Local Similarity 98.8%; Pred. No. 1,1e-45;
Matches 79; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 148 VIAGIRETEEKFYIYVOEKNYRESLTHCRIRGGMAMPKDEAANTLIADYVAKSGFRV 207

QY 61 FIGVNDLEREGQWMTDNT 80
Db 208 FIGVNDLEREGQWMTDNT 227

RESULT 7
ABU87997
ID ABU87997 standard; protein; 277 AA.
XX AC ABU87997;
XX DT 07-JUL-2003 (first entry)
XX DE Novel human secreted and transmembrane protein PRO702.
XX KW Human; secreted and transmembrane protein: PRO; gene therapy;
XX KW tumour necrosis factor-alpha release; TNF-alpha release;
XX KW chondrocyte proliferation; chondrocyte differentiation; tumour;
XX KW adrenal tumour; lung tumour; colon tumour; breast tumour;
XX KW prostate tumour; rectal tumour; cervical tumour; liver tumour.
XX OS Homo sapiens.
XX PN US2003032127-A1.
XX PD 13-FEB-2003.
XX PF 26-JUN-2002; 2002US-00183012.
XX PR 18-SEP-1997; 97US-0059263P.
XX PR 18-SEP-1997; 97US-0059466P.
XX PR 17-OCT-1997; 97US-0062250P.
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PR 11-DEC-1997; 97US-0069335P.
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DB 208 FIGVNDLEREGYMFDTNTP 227

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XX 05-AUG-2003 (first entry)

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XX Human; PRO; secreted protein; transmembrane protein;  
extracellular domain; tumour necrosis factor-alpha; TNF-alpha;  
chondrocyte; proliferation; differentiation; cartilage disorder;  
bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;  
adrenal tumour; lung; colon; breast; prostate; kidney; cervix;  
liver; drug screening; transgenic animal; genetic analysis;  
antiarthritic; vulnery; gene therapy.

XX Homo sapiens.

XX US2003036159-A1.

XX 20-FEB-2003.

XX 02-JUL-2002; 2002US-00188773.

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XX  
DT 27-JUN-2003 (first entry)  
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DE Human PRO polypeptide #50.  
XX  
KW Human; PRO polypeptide; secreted and transmembrane protein; tumour;  
XX chromosome mapping; gene mapping; cytostatic.  
XX Homo sapiens.  
XX  
PN US2003032113-A1.  
XX  
PD 13-FEB-2003.  
XX  
PF 20-JUN-2002; 2002US-00176911.  
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Best Local Similarity 98.8%; Pred. NO. 1.le-45;
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XX DT 11-AUG-2003 (first entry)
XX DE Novel human secreted and transmembrane protein PRO702.
XX KW Human; gene therapy; tissue typing; tumour; chondrocyte proliferation;
XX KW chondrocyte differentiation; tumour necrosis factor-alpha release;
XX KW affinity purification.
XX OS Homo sapiens.
XX PN US2003036147-A1.
XX PD 20-FEB-2003.
XX PF 02-JUL-2002; 2002US-00187741.
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Run on: March 8, 2004, 12:11:31 ; Search time 28.9987 Seconds

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584,534 Million cell updates/sec

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; TITLE OF INVENTION: NO. US20030158382A1el Collectin  
; FILE REFERENCE: 19036/38785  
; CURRENT APPLICATION NUMBER: US/10/258,105  
; CURRENT FILING DATE: 2002-10-21  
; PRIOR APPLICATION NUMBER: PCT/JP01/03468  
; PRIOR FILING DATE: 2001-04-23  
; PRIOR APPLICATION NUMBER: JP 2000-120358  
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; OTHER INFORMATION: for searching EST data base.  
US-10-258-105-14

Query Match 100.0%; Score 417; DB 14; Length 159;  
Best Local Similarity 100.0%; Pred. NO. 2e-45; Indels 0; Gaps 0;  
Matches 80; Conservative 0; Mismatches 0;  
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Db 30 VIAGIRETEKFFYIVQEKKNYRESLTHCRIRGGLAMPKDEAANTLIADYVAKSGFFRV 89  
QY 61 FIGVNDLEREGQYMTDNT 80  
Db 90 FIGVNDLEREGQYMTDNT 109

#### RESULT 2

US-09-978-295A-97  
; Sequence 97, Application US/09978295A  
; Patent No. US2002015606A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
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; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kjavlin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James;  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2630P1C11  
; CURRENT APPLICATION NUMBER: US/09/978,295A  
; CURRENT FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: 09/918585  
; PRIOR FILING DATE: 2001-07-30  
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;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 98.1%; Score 409; DB 9; Length 277;  
Best Local Similarity 98.8%; Pred. No. 4.3e-44;  
Matches 79; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
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Db 148 VIAGIRETEKEKYIVQEKYVRESLTHCRIRGGMLAMPKDEAANTLIADYVAKSGFRV 207  
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QY 61 FIGVNDLEREGYMTDNTP 80  
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Db 208 FIGVNDLEREGYMTDNTP 227  
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RESULT 3  
US-09-978-697-97  
; Sequence 97, Application US/09978697  
; Patent No. US20020169284A1

;; GENERAL INFORMATION:  
;; APPLICANT: Ashkenazi, Avi  
;; APPLICANT: Baker Kevin P.  
;; APPLICANT: Botstein, David  
;; APPLICANT: Deanoyers, Luc  
;; APPLICANT: Eaton, Dan  
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;; APPLICANT: Williams, P. Mickey  
;; APPLICANT: Wood, William I.  
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
;; FILE REFERENCE: P2630PIC27  
;; CURRENT APPLICATION NUMBER: US/09/978,697  
;; CURRENT FILING DATE: 2001-10-16  
;; PRIOR APPLICATION NUMBER: 09/918585  
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 ; PRIOR APPLICATION NUMBER: 60/085697

Query Match 98.1%; Score 409; DB 9; Length 277;

Best Local Similarity 98.8%; Pred. No. 4.3e-44; Matches 79; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VIAGIRETEEFYIVQEKYRESLTHCRIRGKMLPKDEAAANTLIADYVAKSGPFRV 60  
 Db 148 VIAGIRETEEFYIVQEKYRESLTHCRIRGKMLPKDEAAANTLIADYVAKSGPFRV 207  
 Qy 61 FIGVNDLREGGQYNDTNP 80  
 Db 208 FIGVNDLREGGQYNDTNP 227

RESULT 4

US-09-978-192A-97  
 ; Sequence 97, Application US/09978192A  
 ; Patent No. US2002017753A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ashkenazi, Avi  
 ; APPLICANT: Baker Kevin P.



APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
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APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630P1C9  
CURRENT APPLICATION NUMBER: US/09/978,192A  
CURRENT FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: 09/918585  
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 PRIOR APPLICATION NUMBER: 60/085704  
 PRIOR FILING DATE: 1998-05-15  
 PRIOR APPLICATION NUMBER: 60/085697

Query Match 98.1%; Score 409; DB 9; Length 277;  
 Best Local Similarity 98.8%; Pred. No. 4.3e-44;  
 Matches 79; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VIAGIRTESEKYYIVOEKNYRESLTHCRIRGGLAMPKDEAANTLIADYVAKSGPFRV 60  
 Db 148 VIAGIRTESEKYYIVOEKNYRESLTHCRIRGGLAMPKDEAANTLIADYVAKSGPFRV 207  
 Qy 61 FIGVNDLEREGQYMTDNTTP 80  
 Db 208 FIGVNDLEREGQYMTDNTTP 227

RESULT 5  
 US-09-999-832A-97  
 ; Sequence 97, Application US/09999832A  
 ; Publication No. US20020192706A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ashkenazi, Avi  
 ; APPLICANT: Baker Kevin P.  
 ; APPLICANT: Botstein, David  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Eaton, Dan

APPLICANT: Ferrara, Napoleon  
 APPLICANT: Filvaroff, Ellen  
 APPLICANT: Fong, Sherman  
 APPLICANT: Gao, Wei-Qiang  
 APPLICANT: Gerber, Hanspeter  
 APPLICANT: Gerritsen, Mary E.  
 APPLICANT: Goddard, Audrey  
 APPLICANT: Godowski, Paul J.  
 APPLICANT: Grimaldi, J. Christopher  
 APPLICANT: Gurney, Austin L.  
 APPLICANT: Hillan, Kenneth J.  
 APPLICANT: Kljavin, Ivar J.  
 APPLICANT: Kuo, Sophia S.  
 APPLICANT: Napier, Mary A.  
 APPLICANT: Pan, James  
 APPLICANT: Paoni, Nicholas F.  
 APPLICANT: Roy, Margaret Ann  
 APPLICANT: Shelton, David L.  
 APPLICANT: Stewart, Timothy A.  
 APPLICANT: Tumas, Daniel  
 APPLICANT: Williams, P. Mickey  
 APPLICANT: Wood, William I.  
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 FILE REFERENCE: P2630PIC63  
 CURRENT APPLICATION NUMBER: US/09/999,832A  
 CURRENT FILING DATE: 2001-10-24  
 PRIOR APPLICATION NUMBER: 09/918585  
 PRIOR FILING DATE: 2001-07-30  
 PRIOR APPLICATION NUMBER: 60/062250  
 PRIOR FILING DATE: 1997-10-17  
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QY 1 VIAGIRETEKFFYIVQEKYRESLTHCRIGMPLAMPKDEAANTLIADYVAKSGFFRV 60

Db 148 VIAGIRETEKFFYIVQEKYRESLTHCRIGMPLAMPKDEAANTLIADYVAKSGFFRV 207

QY 61 FIGVNDLEREGQYMTDNTIP 80

Db 208 FIGVNDLEREGQYMTDNTIP 227

RESULT 6

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; Sequence 97, Application US/09978189  
; Publication No. US20030004102A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman

APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijavini, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630F1C7  
CURRENT APPLICATION NUMBER: US/09/978,189  
CURRENT FILING DATE: 2001-10-15  
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PRIOR FILING DATE: 2001-07-30  
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PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083559  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083500  
PRIOR FILING DATE: 1998-04-29

GENERAL INFORMATION:

APPLICANT: Asakanezi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botsstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Garber, Hanspeter  
APPLICANT: Gerritsen, Mary E.

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi

APPLICANT: Baker Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnovers, Luc

APPLICANT: Eaton, Dan

APPLICANT: Ferrara, Napoleon

APPLICANT: Filvaroff, Ellen

APPLICANT: Fong, Sherman

APPLICANT: Gao, Wei-Qiang

APPLICANT: Garber, Hanspeter

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Chris

APPLICANT: Gurney, Austin L.

APPLICANT: Hillan, Kenneth J.

APPLICANT: Kijavlin, Ivar J.

APPLICANT: Kuo, Sophia S.

APPLICANT: Napier, Mary A.

APPLICANT: Pan, James

APPLICANT: Pacini, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Shelton, David L.

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Williams, P. Mickle

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APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PIC15
CURRENT APPLICATION NUMBER: US/09/978,585A
CURRENT FILING DATE: 2001-10-16
NUMBER OF SEQ ID NOS: 624
Prior Application removed - See File Wrapper or Palm
SEQ ID NO 97
LENGTH: 277
TYPE: PRT
ORGANISM: Homo sapiens
US-09-978-585A-97

Query Match 98.1%; Score 409; DB 10; Length 277;
Best Local Similarity 98.8%; Pred. No. 4.3e-44;
Matches 79; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VIAGIRETEKFIYVQBEKNTRESLTHCRIRGGMLAMPKDEAANTLIADYVAKSGPFRV 60
Db 148 VIAGIRETEKFIYVQBEKNTRESLTHCRIRGGMLAMPKDEAANTLIADYVAKSGPFRV 207

QY 61 FIGVNDLEREGQMTDNP 80
Db 208 FIGVNDLEREGQMTDNP 227

RESULT 9
US-09-978-191A-97
Sequence 97, Application US/09978,91A
Publication No. US20030050239A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann.
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630PIC4
CURRENT APPLICATION NUMBER: US/09/978,191A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
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DB 148 VIAGIRETEEEKFYIVQBEKNYRESLTHCRIRGGLAMPKDEAANTLIADYVAKSGFFRV 207  
  
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DB 208 FIGVNDLEREGQYMFDTNTP 227  
  
RESULT 10  
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; Sequence 97, Application US/09978403A  
; Publication No. US20030050240A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary B.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kijavir, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2630PIC17  
; CURRENT APPLICATION NUMBER: US/09/978,403A  
; CURRENT FILING DATE: 2002-03-19  
; PRIOR APPLICATION NUMBER: 09/918585  
; PRIOR FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/064249  
; PRIOR FILING DATE: 1997-11-03  
; PRIOR APPLICATION NUMBER: 60/065311  
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[illegible]



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Best Local Similarity 98.8%; Pred. No. 4.3e-44;  
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Db 148 VIAGIRETEKYYIVQEKYRESLTHCRIRGGMLAMPKDEAANTLIADYVAKSGFRV 207

QY 61 FIGVNDLEREGYMTDNT 80

Db 208 FIGVNDLEREGYMTDNT 227

## RESULT 11

US-09-978-564A-97

; Sequence 97, Application US/09978564A

; Publication No. US2003050241A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnovers, Luc

; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleon

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

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; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Kuo, Sophia S.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Shelton, David L.

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; FILE REFERENCE: P2630PIC25

; CURRENT APPLICATION NUMBER: US/09/978,564A

; CURRENT FILING DATE: 2001-10-16

; PRIOR APPLICATION NUMBER: 09/918585

; PRIOR FILING DATE: 2001-07-30

; PRIOR APPLICATION NUMBER: 60/062250

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Db 208 FIGVNDLEREGQYMTDNTTP 227  
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;; Publication No. US20030054405A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Ashkenazi, Avi  
;; APPLICANT: Baker Kevin P.  
;; APPLICANT: Botstein, David  
;; APPLICANT: Desnoyers, Luc  
;; APPLICANT: Eaton, Dan  
;; APPLICANT: Ferrara, Napoleon  
;; APPLICANT: Filvaroff, Ellen  
;; APPLICANT: Fong, Sherman  
;; APPLICANT: Gao, Wei-Qiang  
;; APPLICANT: Gerber, Hanspeter  
;; APPLICANT: Gerritsen, Mary E.  
;; APPLICANT: Goddard, Audrey  
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;; APPLICANT: Grimaldi, J. Christopher  
;; APPLICANT: Gurney, Austin L.  
;; APPLICANT: Hillan, Kenneth J.  
;; APPLICANT: Kijavini, Ivar J.  
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;; APPLICANT: Napier, Mary A.  
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;; APPLICANT: Paoni, Nicholas F.  
;; APPLICANT: Roy, Margaret Ann  
;; APPLICANT: Shelton, David L.  
;; APPLICANT: Stewart, Timothy A.  
;; APPLICANT: Tumas, Daniel  
;; APPLICANT: Williams, P. Mickey  
;; APPLICANT: Wood, William I.  
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
;; FILE REFERENCE: P2630PIC65  
;; CURRENT APPLICATION NUMBER: US/09/999.833A  
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PRIOR FILING DATE: 1998-05-13	PRIOR APPLICATION NUMBER: 60/085323
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; PRIOR APPLICATION NUMBER: 60/085697
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Matches 79; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db 148 VIAGIRETEKYYIVQEBKNTRESLTICRIRGGLAMPKDEAANTLIADYVAKSGFFRV 207
QY 61 FIGVNDLEREGQYMFDTNTP 80
Db 208 FIGVNDLEREGQYMSDTNTP 227
RESULT 13
US-09-981-915A-97
; Sequence 97, Application US/09981915A
; Publication No. US20030054986A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
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; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC12
; CURRENT APPLICATION NUMBER: US/09/981,915A
; CURRENT FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
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Query Match 98.1%; Score 409; DB 10; Length 277;

Best Local Similarity 98.8%; Pred. No. 4.3e-44;  
Matches 79; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
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Db 148 VIAGIRETEEEKFYIVQBEKNYRESLTHCIRGGLAMPKDEAANTLIADYVAKSGFFRV 207  
QY 51 FIGVNDLEREQYMTDNT 80  
Db 208 FIGVNDLEREQYMTDNT 227  
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US-09-978-824-97  
; Sequence 37, Application US/09978824  
; Publication No. US20030055216A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
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; APPLICANT: Grimaldi, J. Christopher  
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; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2630P1C14  
; CURRENT APPLICATION NUMBER: US/09/978,824  
; CURRENT FILING DATE: 2001-10-17  
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Query Match 98.1%; Score 409; DB 10; Length 277;  
Best Local Similarity 98.8%; Pred. No. 4.3e-44;  
Matches 79; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VIAGIRETEKPYIVQEKNYRESLTHCRIRGGMLAMPKDEAANTLIADYVAKSGFRV 60  
Db 148 VIAGIRETEKPYIVQEKNYRESLTHCRIRGGMLAMPKDEAANTLIADYVAKSGFRV 207  
QY 61 FIGVNDLEREGYMTDNTP 80  
Db 208 FIGVNDLEREGYMTDNTP 227

## RESULT 15

US-09-918-585A-97

Sequence 97, Application US/09918585A

Publication No. US20030060406A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi

APPLICANT: Baker Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan

APPLICANT: Ferrara, Napoleon

APPLICANT: Filvaroff, Ellen

APPLICANT: Fong, Sherman

APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary E.

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APPLICANT: Godowski, Paul J.

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APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Shelton, David L.

APPLICANT: Stewart, Timothy A.

APPLICANT: Steward, Daniel

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

Acids Encoding the Same

FILE REFERENCE: P2630P1C1

CURRENT APPLICATION NUMBER: US/09/918,585A

CURRENT FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: 60/062250

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63 PRIOR APPLICATION NUMBER: 60/085697  
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148 VIAGIRETEKFFYVQEEKYVESLTHCRIRGGMLAMPKDEAANTLIADYVAKSGPRV 207

Oy 61 FIGVNDLREGQYMFDTNTP 80  
Db 208 FIGVNDLREGQYMFDTNTP 227

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